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# OM protein - protein search, using sw model

Run on: January 18, 2006, 20:50:17 : Search time 129 Seconds  
(without alignments)  
34.060 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 10  
Sequence: 1 EYLVPPQGP 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 556551

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database :

A\_Geneseq\_21:\*

- 1: geneseqp19808:\*
- 2: geneseqp19808:\*
- 3: geneseqp20008:\*
- 4: geneseqp20018:\*
- 5: geneseqp20028:\*
- 6: geneseqp20038:\*
- 7: geneseqp20048:\*
- 8: geneseqp20058:\*
- 9: geneseqp20068:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	100.0	100.0	10	AAE20480	Naturally
2	100.0	100.0	10	AAU77115	Human Her
3	100.0	100.0	10	ADN64634	HLA bindi
4	100.0	100.0	10	ADP80240	Human HLA
5	90.0	90.0	9	ADM12634	MHC class
6	90.0	90.0	9	ADN64592	HLA bindi
7	90.0	90.0	9	ADN64592	HLA bindi
8	90.0	90.0	9	ADN64592	HLA bindi
9	90.0	90.0	9	ADN64592	HLA bindi
10	90.0	90.0	9	ADN64592	HLA bindi
11	90.0	90.0	9	ADN64592	HLA bindi
12	90.0	90.0	9	ADN64592	HLA bindi
13	90.0	90.0	9	ADN64592	HLA bindi
14	90.0	90.0	9	ADN64592	HLA bindi
15	90.0	90.0	9	ADN64592	HLA bindi
16	90.0	90.0	9	ADN64592	HLA bindi
17	90.0	90.0	9	ADN64592	HLA bindi
18	90.0	90.0	9	ADN64592	HLA bindi
19	90.0	90.0	9	ADN64592	HLA bindi
20	90.0	90.0	9	ADN64592	HLA bindi
21	90.0	90.0	9	ADN64592	HLA bindi
22	90.0	90.0	9	ADN64592	HLA bindi
23	90.0	90.0	9	ADN64592	HLA bindi
24	90.0	90.0	9	ADN64592	HLA bindi

25	40.0	6	AAU80407	Positive
26	40.0	7	AAE23680	Cyclic hi
27	40.0	7	AAE23681	Cyclic hi
28	40.0	7	AAE23681	Cyclic hi
29	40.0	7	AAE23681	Cyclic hi
30	40.0	7	AAE23681	Cyclic hi
31	40.0	7	AAE23681	Cyclic hi
32	40.0	7	AAE23681	Cyclic hi
33	40.0	7	AAE23681	Cyclic hi
34	40.0	7	AAE23681	Cyclic hi
35	40.0	7	AAE23681	Cyclic hi
36	40.0	7	AAE23681	Cyclic hi
37	40.0	7	AAE23681	Cyclic hi
38	40.0	7	AAE23681	Cyclic hi
39	40.0	7	AAE23681	Cyclic hi
40	40.0	7	AAE23681	Cyclic hi
41	40.0	7	AAE23681	Cyclic hi
42	40.0	7	AAE23681	Cyclic hi
43	40.0	7	AAE23681	Cyclic hi
44	40.0	7	AAE23681	Cyclic hi
45	40.0	7	AAE23681	Cyclic hi
46	40.0	7	AAE23681	Cyclic hi
47	40.0	7	AAE23681	Cyclic hi
48	40.0	7	AAE23681	Cyclic hi
49	40.0	7	AAE23681	Cyclic hi
50	40.0	7	AAE23681	Cyclic hi
51	40.0	7	AAE23681	Cyclic hi
52	40.0	7	AAE23681	Cyclic hi
53	40.0	7	AAE23681	Cyclic hi
54	40.0	7	AAE23681	Cyclic hi
55	40.0	7	AAE23681	Cyclic hi
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57	40.0	7	AAE23681	Cyclic hi
58	40.0	7	AAE23681	Cyclic hi
59	40.0	7	AAE23681	Cyclic hi
60	40.0	7	AAE23681	Cyclic hi
61	40.0	7	AAE23681	Cyclic hi
62	40.0	7	AAE23681	Cyclic hi
63	40.0	7	AAE23681	Cyclic hi
64	40.0	7	AAE23681	Cyclic hi
65	40.0	7	AAE23681	Cyclic hi
66	40.0	7	AAE23681	Cyclic hi
67	40.0	7	AAE23681	Cyclic hi
68	40.0	7	AAE23681	Cyclic hi
69	40.0	7	AAE23681	Cyclic hi
70	40.0	7	AAE23681	Cyclic hi
71	40.0	7	AAE23681	Cyclic hi
72	40.0	7	AAE23681	Cyclic hi
73	40.0	7	AAE23681	Cyclic hi
74	40.0	7	AAE23681	Cyclic hi
75	40.0	7	AAE23681	Cyclic hi
76	40.0	7	AAE23681	Cyclic hi
77	40.0	7	AAE23681	Cyclic hi
78	40.0	7	AAE23681	Cyclic hi
79	40.0	7	AAE23681	Cyclic hi
80	40.0	7	AAE23681	Cyclic hi
81	40.0	7	AAE23681	Cyclic hi
82	40.0	7	AAE23681	Cyclic hi
83	40.0	7	AAE23681	Cyclic hi
84	40.0	7	AAE23681	Cyclic hi
85	40.0	7	AAE23681	Cyclic hi
86	40.0	7	AAE23681	Cyclic hi
87	40.0	7	AAE23681	Cyclic hi
88	40.0	7	AAE23681	Cyclic hi
89	40.0	7	AAE23681	Cyclic hi
90	40.0	7	AAE23681	Cyclic hi
91	40.0	7	AAE23681	Cyclic hi
92	40.0	7	AAE23681	Cyclic hi
93	40.0	7	AAE23681	Cyclic hi
94	40.0	7	AAE23681	Cyclic hi
95	40.0	7	AAE23681	Cyclic hi
96	40.0	7	AAE23681	Cyclic hi
97	40.0	7	AAE23681	Cyclic hi

98	4	40.0	9	7	ABW00532	Abw00532 Human cyt	171	4	40.0	10	2	AAV46515	AAy46515 Immunogen
99	4	40.0	9	7	ABW00531	Abw00531 Human cyt	172	4	40.0	10	3	AAW49127	AAW49127 Hepatitis
100	4	40.0	9	7	ABW00564	Abw00564 Human cyt	173	4	40.0	10	3	AAV53096	AAV53096 Anticoagu
101	4	40.0	9	7	ABW00555	Abw00555 Human cyt	174	4	40.0	10	3	AAV53084	AAV53084 Anticoagu
102	4	40.0	9	7	ABW00566	Abw00566 Human cyt	175	4	40.0	10	3	AAV53066	AAV53066 Anticoagu
103	4	40.0	9	7	ABW00553	Abw00553 Human cyt	176	4	40.0	10	3	AAV53100	AAV53100 Anticoagu
104	4	40.0	9	7	ABW00556	Abw00556 Human cyt	177	4	40.0	10	3	AAV53069	AAV53069 Anticoagu
105	4	40.0	9	7	ABW00563	Abw00563 Human cyt	178	4	40.0	10	3	AAV53105	AAV53105 Anticoagu
106	4	40.0	9	7	ABW32935	Adw32935 HLA bindi	179	4	40.0	10	3	AAV73049	AAV73049 Hepatitis
107	4	40.0	9	8	ADW37700	Adw37700 Immunogen	180	4	40.0	10	3	AAW14923	AAW14923 Random 27
108	4	40.0	9	8	ADW37686	Adw37686 Immunogen	181	4	40.0	10	4	AAW06547	AAW06547 Forythia
109	4	40.0	9	8	ADK38445	Adk38445 Hepatitis	182	4	40.0	10	4	AAU24412	AAU24412 Human MHC
110	4	40.0	9	8	ADK37830	Adk37830 Hepatitis	183	4	40.0	10	4	AAU24276	AAU24276 Human MHC
111	4	40.0	9	8	ADK39150	Adk39150 Hepatitis	184	4	40.0	10	4	AAU23979	AAU23979 Human MHC
112	4	40.0	9	8	ADK32485	Adk32485 Hepatitis	185	4	40.0	10	4	AAU24282	AAU24282 Human MHC
113	4	40.0	9	8	ADK04911	Adk04911 Hepatitis	186	4	40.0	10	4	AAU24404	AAU24404 Human MHC
114	4	40.0	9	8	ADM78176	Adm78176 Hepatitis	187	4	40.0	10	4	AAU24404	AAU24404 Human MHC
115	4	40.0	9	8	ADO17559	Ado17559 Different	188	4	40.0	10	4	AAU24288	AAU24288 Human MHC
116	4	40.0	9	8	ADO17225	Ado17225 Different	189	4	40.0	10	5	AAE28763	AAE28763 Human CNS
117	4	40.0	9	8	ADO17510	Ado17510 Different	190	4	40.0	10	5	ABJ09870	ABJ09870 Hepatitis
118	4	40.0	9	8	ADO17530	Ado17530 Different	191	4	40.0	10	5	ABJ10131	ABJ10131 Hepatitis
119	4	40.0	9	8	ADO24039	Ado24039 HBV epito	192	4	40.0	10	5	ABJ10181	ABJ10181 Hepatitis
120	4	40.0	9	8	ADO23899	Ado23899 HBV HLA-A	193	4	40.0	10	5	ABJ10038	ABJ10038 Hepatitis
121	4	40.0	9	8	ADO01421	Ado01421 Human cyt	194	4	40.0	10	5	ABJ10081	ABJ10081 Hepatitis
122	4	40.0	9	8	ADO01432	Ado01432 Human cyt	195	4	40.0	10	5	ABJ09598	ABJ09598 Hepatitis
123	4	40.0	9	8	ADO01425	Ado01425 Human cyt	196	4	40.0	10	5	ABJ07090	ABJ07090 Hepatitis
124	4	40.0	9	8	ADO01399	Ado01399 Human cyt	197	4	40.0	10	5	ABJ08626	ABJ08626 Hepatitis
125	4	40.0	9	8	ADO01400	Ado01400 Human cyt	198	4	40.0	10	5	ABJ06551	ABJ06551 Hepatitis
126	4	40.0	9	8	ADO01433	Ado01433 Human cyt	199	4	40.0	10	6	ABR21075	ABR21075 Human can
127	4	40.0	9	8	ADO01434	Ado01434 Human cyt	200	4	40.0	10	6	ABR22655	ABR22655 Human can

## ALIGNMENTS

RESULT 1  
ID AAE20480 standard; peptide; 10 AA.  
AAE20480;

AC AAE20480; (first entry)  
XX 01-JUL-2002  
XX Naturally processed HLA-B\*44-restricted epitope of human Her-2/neu.  
XX Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
XX human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX Homo sapiens.  
XX WO200214503-A2.  
XX 21-FEB-2002.  
XX 14-AUG-2001; 2001WO-US041733.  
XX 14-AUG-2000; 2000US-0225152P.  
XX 28-SEP-2000; 2000US-0236428P.  
XX 21-FEB-2001; 2001US-0270520P.  
XX (CORI-) CORIXA CORP.  
XX Hand-Zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
XX McNeill PD, Vedrick TS;  
XX WPI; 2002-280758/32.  
XX Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
XX prevention and diagnosis of cancer, preferably breast cancer.  
XX Claim 2; Page 87; 12pp; English.  
XX The invention relates to an isolated Her-2/Neu polypeptide composition  
XX CC

98	4	40.0	9	7	ABW00532	Abw00532 Human cyt
99	4	40.0	9	7	ABW00531	Abw00531 Human cyt
100	4	40.0	9	7	ABW00564	Abw00564 Human cyt
101	4	40.0	9	7	ABW00555	Abw00555 Human cyt
102	4	40.0	9	7	ABW00566	Abw00566 Human cyt
103	4	40.0	9	7	ABW00553	Abw00553 Human cyt
104	4	40.0	9	7	ABW00556	Abw00556 Human cyt
105	4	40.0	9	7	ABW00563	Abw00563 Human cyt
106	4	40.0	9	7	ABW32935	Adw32935 HLA bindi
107	4	40.0	9	8	ADW37700	Adw37700 Immunogen
108	4	40.0	9	8	ADW37686	Adw37686 Immunogen
109	4	40.0	9	8	ADK38445	Adk38445 Hepatitis
110	4	40.0	9	8	ADK37830	Adk37830 Hepatitis
111	4	40.0	9	8	ADK39150	Adk39150 Hepatitis
112	4	40.0	9	8	ADK32485	Adk32485 Hepatitis
113	4	40.0	9	8	ADK04911	Adk04911 Hepatitis
114	4	40.0	9	8	ADM78176	Adm78176 Hepatitis
115	4	40.0	9	8	ADO17559	Ado17559 Different
116	4	40.0	9	8	ADO17225	Ado17225 Different
117	4	40.0	9	8	ADO17510	Ado17510 Different
118	4	40.0	9	8	ADO17530	Ado17530 Different
119	4	40.0	9	8	ADO24039	Ado24039 HBV epito
120	4	40.0	9	8	ADO23899	Ado23899 HBV HLA-A
121	4	40.0	9	8	ADO01421	Ado01421 Human cyt
122	4	40.0	9	8	ADO01432	Ado01432 Human cyt
123	4	40.0	9	8	ADO01425	Ado01425 Human cyt
124	4	40.0	9	8	ADO01399	Ado01399 Human cyt
125	4	40.0	9	8	ADO01400	Ado01400 Human cyt
126	4	40.0	9	8	ADO01433	Ado01433 Human cyt
127	4	40.0	9	8	ADO01434	Ado01434 Human cyt
128	4	40.0	9	8	ADO01423	Ado01423 Human cyt
129	4	40.0	9	8	ADO01424	Ado01424 Human cyt
130	4	40.0	9	8	ADO01431	Ado01431 Human cyt
131	4	40.0	9	8	ADO01432	Ado01432 Human cyt
132	4	40.0	9	8	ADO01426	Ado01426 Human cyt
133	4	40.0	9	8	ADO12318	Adq12318 Hepatitis
134	4	40.0	9	8	ADO12314	Adq12314 Hepatitis
135	4	40.0	9	8	ADO12317	Adq12317 Hepatitis
136	4	40.0	9	8	ADO12316	Adq12316 Hepatitis
137	4	40.0	9	8	ADO12313	Adq12313 Hepatitis
138	4	40.0	9	8	ADO12315	Adq12315 Hepatitis
139	4	40.0	9	8	ADR23509	Adr23509 Human thr
140	4	40.0	9	8	ADR23510	Adr23510 Human thr
141	4	40.0	9	8	ADR23479	Adr23479 Human thr
142	4	40.0	9	8	ADR23508	Adr23508 Human thr
143	4	40.0	9	8	ADY98702	Ady98702 TYE assoc
144	4	40.0	9	8	ABY01304	AbY01304 SARS coro
145	4	40.0	9	9	ADW22953	Adw22953 SARS coro
146	4	40.0	9	9	ADW57828	Adw57828 G protein
147	4	40.0	9	9	ADW71145	Adw71145 Mouse tum
148	4	40.0	9	9	ADZ05835	Adz05835 Hepatitis
149	4	40.0	9	9	ADZ05220	Adz05220 Hepatitis
150	4	40.0	9	9	ADZ06540	Adz06540 Hepatitis
151	4	40.0	9	9	ADZ40426	Adz40426 HBV vacci
152	4	40.0	9	9	ADZ40448	Adz40448 HBV vacci
153	4	40.0	9	9	ADZ40859	Adz40859 HBV Epige
154	4	40.0	9	9	ADZ40524	Adz40524 HBV vacci
155	4	40.0	9	9	ADZ40441	Adz40441 HBV vacci
156	4	40.0	9	9	ADZ50139	Adz50139 Y. pestis
157	4	40.0	9	9	ADZ56790	Adz56790 Cytoxic
158	4	40.0	10	1	AAW50992	AAW50992 Cholecyat
159	4	40.0	10	1	AAW50993	AAW50993 Cholecyat
160	4	40.0	10	2	AAW13532	AAW13532 Hirtudin-d
161	4	40.0	10	2	AAW33689	AAW33689 Cyclic hl
162	4	40.0	10	2	AAW33674	AAW33674 Hirtudin d
163	4	40.0	10	2	AAW39928	AAW39928 N-termina
164	4	40.0	10	2	AAW39926	AAW39926 N-termina
165	4	40.0	10	2	AAW18020	AAW18020 Hirtudin C
166	4	40.0	10	2	AAW61560	AAW61560 Peptidic f
167	4	40.0	10	2	AAW92928	AAW92928 Hirtudin p
168	4	40.0	10	2	AAW55034	AAW55034 Forythia
169	4	40.0	10	2	AAW46031	AAW46031 Immunogen
170	4	40.0	10	2	AAW46440	AAW46440 Immunogen

CC effective for eliciting an immune response. The invention is useful for  
 CC eliciting an immune response in a patient, where the patient is human  
 CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
 CC The composition is useful for the therapy and diagnosis of cancer,  
 CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
 CC and other compositions for the diagnosis, prevention and treatment of  
 CC human malignancies, for stimulating and/or expanding T cells specific for  
 CC Her-2/neu polypeptide and for inhibiting the development of cancer in a  
 CC patient. The invention is useful for stimulating a T cell response in a  
 CC human patient, as probe or primer for nucleic acid hybridisation, to  
 CC selectively form duplex molecules with complementary stretches of the  
 CC entire Her-2/neu gene or gene fragments of interest, to isolate a full  
 CC length gene from a suitable library, and to direct expression of a  
 CC polypeptide in appropriate host cells. The composition is useful in  
 CC prophylactic or therapeutic applications and for the treatment of cancer,  
 CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
 CC associated malignancies. The invention is useful in gene therapy. The  
 CC present sequence is naturally processed HLA-B44-restricted epitope of  
 CC human Her-2/neu protein

CC Sequence 10 AA;

Query Match 100.0%; Score 10; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 |||||  
 Db 1 EEYLVPOQGF 10

RESULT 2  
 AAU77115  
 ID AAU77115 standard; peptide; 10 AA.

XX AAU77115;

XX 05-JUN-2002 (first entry)

XX Human Her-2/neu immunogenic epitope.

XX Human; Her-2/neu; cytostatic; haematological malignancy; CML;

XX acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;

XX chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;

XX Hodgkin's lymphoma; T cell therapy.

XX Homo sapiens.

XX WO200213847-A2.

XX 21-FEB-2002.

XX 13-AUG-2001; 2001WO-US025408.

XX 14-AUG-2000; 2000US-00638280.

XX 28-SEP-2000; 2000US-00675904.

XX (COR-) CORIXA CORP.

XX Gaiger A, Cheever MA, Hand-Zimmermann S;

XX WPI, 2002-280741/32.

XX Inhibiting hematological malignancy development by administering

XX polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide

XX encoding the polypeptide, or antigen presenting cells expressing the

XX polypeptide.

XX Claim 2; Page 49; 74pp; English.

XX The invention relates to a method for inhibiting development of

XX haematological malignancy in a patient by administering a polypeptide

XX comprising an immunogenic portion of Her-2/neu or a polynucleotide

CC encoding the polypeptide. Antigen presenting cells that express the  
 CC protein can also be administered. The sequences are used for inhibiting  
 CC development of hematological malignancy such as acute myelogenous  
 CC leukaemia (AML), chronic myelogenous leukaemia (CM), chronic lymphocytic  
 CC leukaemia (CLL), MDS, myeloma, Hodgkin's lymphoma and non-Hodgkin's  
 CC lymphoma. This sequence represents a human Her-2/neu immunogenic epitope

CC Sequence 10 AA;

Query Match 100.0%; Score 10; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 |||||  
 Db 1 EEYLVPOQGF 10

RESULT 3  
 ADN64634  
 ID ADN64634 standard; peptide; 10 AA.

XX ADN64634;

XX 01-JUL-2004 (first entry)

XX HLA binding peptide #1234.

XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;

XX gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;

XX prostate specific antigen; prostate specific membrane antigen;

XX hepatitis B virus antigen; hepatitis C virus antigen;

XX malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;

XX prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;

XX chondyoma acuminatum.

XX Unidentified.

XX WO2004031211-A2.

XX 15-APR-2004.

XX 03-OCT-2003; 2003WO-US031308.

XX 03-OCT-2002; 2002US-0416207P.

XX 08-OCT-2002; 2002US-0417269P.

XX (EPIM-) EPIMUNE INC.

XX Sidney J, Southwood S, Sette A;

XX WPI, 2004-347953/32.

XX New composition of peptides and nucleic acids capable of binding Major

XX Histocompatibility Complex molecules, useful for diagnosing, preventing

XX or treating viral infections or cancer, such as prostate cancer,

XX hepatitis B or AIDS.

XX Claim 1; SEQ ID NO 1234; 186pp; English.

XX The invention relates to a novel composition comprising one or more

XX peptides or nucleic acids encoding an HLA binding peptide. The

XX composition further comprises an HTL epitope. It also comprises a spacer

XX molecule, a carrier, an MHC targeting sequence or a lipid. The peptides

XX are incorporated as part of a liposome. The peptide is from an antigen

XX selected from prostate specific antigen (PSA), prostate specific membrane

XX antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)

XX antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human

XX immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),

XX Papilloma virus, Laesa virus, Mycobacterium tuberculosis (MT), p53,

XX murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein

XX (TKP). The composition is useful for preventing or treating viral

XX infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,

CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyroma  
 CC acuminatum. The composition is also be used for diagnosing such diseases.  
 CC This sequence represents a peptide of the invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
 |||||  
 DB 1 EYLVPOQGF 10

RESULT 4  
 ADP80240  
 ID ADP80240 standard; peptide; 10 AA.  
 XX  
 AC ADP80240;  
 XX  
 DT 18-NOV-2004 (first entry)

DE Human HLA-B44 epitope vaccine peptide SegID496.

XX epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;  
 KW tumour associated antigen peptide; cytostatic; vaccine; human.

XX Homo sapiens.

XX WO2004052917-A2.

XX 24-JUN-2004.

XX 10-DEC-2003; 2003WO-US038949.

XX 10-DEC-2002; 2002US-0432017P.

XX (EPIM-) EPIMUNE INC.

XX Keogh EA, Southwood S, Fikes JD, Sette A;

XX WPI; 2004-468809/44.

PT New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,  
 PT useful in preparing a composition for diagnosing or treating tumor  
 PT associated antigen-related disease.

XX Claim 1; SEQ ID NO 496; 244pp; English.

XX This invention relates to a novel isolated peptide which comprises at  
 CC least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given  
 CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or  
 CC B44 tumour associated antigen peptide. The invention may be useful for  
 CC the production of compounds with a cytostatic activity or for the  
 CC production of a vaccine. The peptide is useful in preparing a composition  
 CC diagnosing or treating tumour associated antigen-related disease. The  
 CC present sequence is that of an epitope peptide for use in the peptide of  
 CC the invention.  
 XX

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
 |||||  
 DB 1 EYLVPOQGF 10

RESULT 5  
 ADM12634

ID ADM12634 standard; peptide; 9 AA.

XX ADM12634;

XX 20-MAY-2004 (first entry)

DE MHC class I epitope of human Her-2/neu, 16-5-6.

XX antigen presentation enhancing hybrid polypeptide; mammalian II-Key;  
 KW MHC class II; antibacterial; virucide; fungicide; antirheumatic;  
 KW antiarthritic; neuroprotective; dermatological; immunosuppressive;  
 KW antiinflammatory; antidiabetic; antihypoid; immune;  
 KW rheumatoid arthritis; multiple sclerosis; lupus erythematosus;  
 KW diabetes mellitus; myasthenia gravis; autoimmune thyroiditis;  
 KW scleroderma; dermatomyositis; pemphigus.

XX Homo sapiens.

XX US2003235594-A1.

XX 25-DEC-2003.

XX 17-SEP-2002; 2002US-00245871.

XX 14-SEP-1999; 99US-00396813.

XX 17-JUL-2002; 2002US-00197000.

XX (ANTI-) ANTIGEN EXPRESS INC.

XX Humphreys R, Xu M;

XX WPI; 2004-070554/07.

PT Novel II-Key/antigen presentation enhancing hybrid polypeptide, useful  
 PT for treating infections, rheumatoid arthritis, multiple sclerosis, lupus  
 PT erythematosus and diabetes mellitus.

XX Example 16; Page 54; 87pp; English.

XX The invention relates to a novel antigen presentation enhancing hybrid  
 CC polypeptide. The novel polypeptide has an N-terminal element consisting  
 CC of 4-16 residues of a mammalian II-key peptide and its non-N-terminal  
 CC deletion modifications, a chemical structure covalently linking the N-  
 CC terminal element to an MHC class II-presented epitope of a C-terminal  
 CC element. The C-terminal element comprises an antigenic epitope, which  
 CC binds to an antigenic peptide binding site of an MHC class II molecule.  
 CC The antigen presentation enhancing hybrid polypeptide has the following  
 CC activities: antibacterial, virucide, fungicide, antirheumatic,  
 CC antiarthritic, neuroprotective, dermatological, immunosuppressive,  
 CC antiinflammatory, antidiabetic, and antihypoid. The antigen presentation  
 CC enhancing hybrid polypeptide is useful for modulating the immune response  
 CC in an individual and for treating infections (such as bacteria, virus,  
 CC parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus  
 CC erythematosus, diabetes mellitus, myasthenia gravis, autoimmune  
 CC thyroiditis, scleroderma, dermatomyositis and pemphigus. This sequence  
 CC represents a mammalian II key related peptide epitope of the invention.  
 XX

XX Sequence 9 AA;

Query Match 90.0%; Score 9; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10  
 |||||  
 DB 1 EYLVPOQGF 9

RESULT 6  
 ADN64592  
 ID ADN64592 standard; peptide; 9 AA.  
 XX  
 AC ADN64592;



XX 01-JUL-2004 (first entry)  
 XX HLA binding peptide #1192.  
 XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;  
 XX gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;  
 XX prostate specific antigen; prostate specific membrane antigen;  
 XX hepatitis B virus antigen; hepatitis C virus antigen;  
 XX malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;  
 XX prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;  
 XX chondroma acuminatum.  
 XX Unidentified.  
 XX WO2004031211-A2.  
 XX 15-APR-2004.  
 XX 03-OCT-2003; 2003WO-US031308.  
 XX 03-OCT-2002; 2002US-0416207P.  
 XX 08-OCT-2002; 2002US-0417269P.  
 XX (EPTM-) EPTMUNE INC.  
 XX Sidney J, Southwood S, Sette A;  
 XX MPI, 2004-347953/32.  
 XX New composition of peptides and nucleic acids capable of binding Major  
 XX Histocompatibility Complex molecules, useful for diagnosing, preventing  
 XX or treating viral infections or cancer, such as prostate cancer,  
 XX hepatitis B or AIDS.  
 XX Claim 1; SEQ ID NO 1192; 186bp; English.  
 XX  
 XX The invention relates to a novel composition comprising one or more  
 XX peptides or nucleic acids encoding an HLA binding peptide. The  
 XX composition further comprises an HTL epitope. It also comprises a spacer  
 XX molecule, a carrier, an MHC targeting sequence or a lipid. The peptides  
 XX are incorporated as part of a liposome. The peptide is from an antigen  
 XX selected from prostate specific antigen (PSA), prostate specific membrane  
 XX antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)  
 XX antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human  
 XX immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),  
 XX Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,  
 XX murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein  
 XX (TKP). The composition is useful for preventing or treating viral  
 XX infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,  
 XX AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondroma  
 XX acuminatum. The composition is also be used for diagnosing such diseases.  
 XX This sequence represents a peptide of the invention.  
 XX  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 90.0%; Score 9; DB 8; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 EBYLVPOQG 9  
 XX 1 EBYLVPOQG 9  
 XX  
 XX RESULT 7  
 XX ADO38867  
 XX ID ADO38867 standard; peptide; 9 AA.  
 XX ADO38867;  
 XX  
 XX 15-JUL-2004 (first entry)

DE Human Her-2/neu MHC class II-presented epitope #54.  
 XX  
 XX Antibacterial; virucide; Fungicide; Antiparasitic; Antiarthritic;  
 XX Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;  
 XX Immunosuppressive; Antidiabetic; Antichyroid; Antiscabetic;  
 XX Antiallergic; Cytostatic; Antipsoiatic; Gene therapy; Vaccine;  
 XX MHC Class II; II-key motif; immune response; anthrax; EBOLA; HIV;  
 XX influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;  
 XX rickettsia; rheumatoid arthritis; multiple sclerosis;  
 XX lupus erythematosus; diabetes mellitus; myasthenia gravis;  
 XX autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; asthma;  
 XX allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;  
 XX adenoma.  
 XX  
 XX Homo sapiens.  
 XX  
 XX US2004058881-A1.  
 XX  
 XX 25-MAR-2004.  
 XX 24-SEP-2002; 2002US-00253286.  
 XX 24-SEP-2002; 2002US-00253286.  
 XX  
 XX (ANTI-) ANTIGEN EXPRESS INC.  
 XX  
 XX Humphreys RE, Xu M;  
 XX MPI, 2004-294259/27.  
 XX  
 XX New non-naturally occurring protein or polypeptide modified by  
 XX recombinant DNA techniques, useful for treating multiple sclerosis,  
 XX diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,  
 XX colitis, cancer or psoriasis.  
 XX  
 XX Example 16; Page 57; 90bp; English.  
 XX  
 XX The invention relates to a non-naturally occurring protein or polypeptide  
 XX (I) modified by recombinant DNA techniques comprising: a C-terminal  
 XX element comprising an MHC Class II-presented epitope; an N-terminal  
 XX element comprising an II-key motif; and an intervening element comprising  
 XX a sequence of 4-11 amino acid residues where the modification by  
 XX recombinant DNA techniques taking place within elements (b) and (c). Also  
 XX described are methods for: suppressing or enhancing an immune response  
 XX directed toward an MHC (major histocompatibility complex) Class II-  
 XX presented epitope of interest. Suppressing an immune response directed  
 XX toward an MHC Class II-presented epitope of interest comprises: providing  
 XX a nucleic acid sequence encoding the MHC Class II-presented epitope of  
 XX interest, the nucleic acid sequence encoding an II-key motif located 4-11  
 XX amino acids upstream from the N-terminal residue of the MHC Class II-  
 XX presented epitope of interest; and modifying the II-key motif to decrease  
 XX its conformance to the archetypal II-key regulatory motif. Enhancing an  
 XX immune response directed toward a nucleic acid sequence encoding the MHC  
 XX Class II-presented epitope of interest, the nucleic acid sequence lacking  
 XX an II-key motif located 4-11 amino acids upstream from the N-terminal  
 XX residue of the MHC Class II-presented epitope of interest; and modifying  
 XX the nucleic acid sequence to introduce an II-key motif appropriately  
 XX spaced from the MHC Class II-presented epitope. The protein or  
 XX polypeptide of interest corresponds to a protein or polypeptide encoded  
 XX by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,  
 XX preferably vaccinia virus. The non-naturally occurring protein or  
 XX polypeptide (II) modified by recombinant DNA techniques is useful for  
 XX treating infectious diseases caused or associated with infection by a  
 XX bacterium, virus, parasite, fungus, rickettsia or other infectious  
 XX agents. It is also useful for treating rheumatoid arthritis, multiple  
 XX sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,  
 XX autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,  
 XX allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or  
 XX adenomas. The present sequence represents the amino acid sequence of an  
 XX MHC class II-presented epitope used in the invention.  
 XX  
 XX Sequence 9 AA;

Query Match 90.0%; Score 9; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10  
|||  
1 EYLVPQGGF 9

## RESULT 8

ID ADP80239 standard; peptide; 9 AA.

AC ADP80239;

DT 18-NOV-2004 (first entry)

DE Human HLA-B44 epitope vaccine peptide SeqID495.

XX epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;  
KW tumour associated antigen peptide; cytostatic; vaccine; human.

XX Homo sapiens.

OS WO2004052917-A2.

PN 24-JUN-2004.

PD 10-DEC-2003; 2003WO-US038949.

PR 10-DEC-2002; 2002US-0432017P.

XX (EPIIM-) EPIIMUNE INC.

PA Keogh EA, Southwood S, Fikes JD, Sette A;

DR WPI; 2004-468809/44.

XX New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,  
PT useful in preparing a composition for diagnosing or treating tumor  
associated antigen-related disease.

PS Claim 1; SEQ ID NO 495; 244bp; English.

XX This invention relates to a novel isolated peptide which comprises at  
CC least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given  
CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or  
CC B44 tumour associated antigen peptide. The invention may be useful for  
CC the production of compounds with a cytostatic activity or for the  
CC production of a vaccine. The peptide is useful in preparing a composition  
CC diagnosing or treating tumour associated antigen-related disease. The  
CC present sequence is that of an epitope peptide for use in the peptide of  
CC the invention.

XX Sequence 9 AA;

Query Match 90.0%; Score 9; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPQGGF 9  
|||  
1 EYLVPQGGF 9

## RESULT 9

ID AAY46040 standard; peptide; 10 AA.

AC AAY46040;

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #651.  
DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
XX immune response; T cell activation; major histocompatibility complex;  
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.

XX Synthetic.

OS Homo sapiens.

XX WO9945954-A1.

PD 16-SEP-1999.

PR 13-MAR-1998; 98WO-US005039.

XX 13-MAR-1998; 98WO-US005039.

PA (EPIIM-) EPIIMUNE INC.

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

DR WPI; 1999-551214/46.

XX New immunogenic peptides with HLA binding motif, useful in treatment and  
PT diagnosis of cancers and viral diseases.

PS Claim 1; Page 53; 150bp; English.

XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
CC having a human major histocompatibility complex (MHC) Class I (also known  
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
CC can bind to a specific HLA allele (i.e. HLA-A subtype HLA-A2.1, A1, A3.2  
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
CC than the intact foreign antigen itself, and are particularly important in  
CC tumour rejection and in fighting viral infections. The peptides are  
CC therefore useful therapeutically to treat or prevent viral infections and  
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
CC elicit an immune response in individuals susceptible or otherwise at risk  
CC of viral infection or cancer, or used to treat chronic or acute  
CC conditions. They are also useful diagnostically, and can be used to  
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
CC patient. The polynucleotides encoding the immunogenic peptides are also  
CC useful therapeutically and for immunisation as above

XX Sequence 10 AA;

Query Match 90.0%; Score 9; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10  
|||  
1 EYLVPQGGF 9

## RESULT 10

ID AAY46513 standard; peptide; 10 AA.

AC AAY46513;

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #1124.

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocytes; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX WO9945954-A1.  
 XX 16-SEP-1999.  
 XX PD  
 XX PF 13-MAR-1998; 98WO-US005039.  
 XX PR 13-MAR-1998; 98WO-US005039.  
 XX PA (EPIM-) EPIMUNE INC.  
 XX PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;  
 XX WPI, 1999-551214/46.  
 XX DR  
 XX PT New immunogenic peptides with HLA binding motif, useful in treatment and  
 XX diagnosis of cancers and viral diseases.  
 XX PS Claim 1, Page 75, 150pp; English.  
 XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 XX having a human major histocompatibility complex (MHC) Class I (also known  
 XX as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
 XX can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
 XX or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
 XX the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
 XX (CTLs) which destroy antigen-bearing cells are normally induced by an  
 XX antigen in the form of a peptide fragment bound to a HLA molecule, rather  
 XX than the intact foreign antigen itself, and are particularly important in  
 XX tumour rejection and in fighting viral infections. The peptides are  
 XX therefore useful therapeutically to treat or prevent viral infections and  
 XX cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
 XX and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
 XX elicit an immune response in individuals susceptible or otherwise at risk  
 XX of viral infection or cancer, or used to treat chronic or acute  
 XX conditions. They are also useful diagnostically, and can be used to  
 XX induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
 XX the peptide e.g. to produce CTLs ex vivo for infusion back into a  
 XX patient. The polynucleotides encoding the immunogenic peptides are also  
 XX useful therapeutically and for immunisation as above  
 XX  
 XX SQ Sequence 10 AA;  
 XX  
 XX Query Match 90.0%; Score 9; DB 2; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 0.0069;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 2 EYLVPQGGF 10  
 XX |||||  
 XX 1 EYLVPQGGF 9  
 XX DB  
 XX  
 XX RESULT 11  
 XX AAY46437  
 XX ID AAY46437 standard; peptide; 10 AA.  
 XX AC AAY46437;  
 XX XX  
 XX DT 01-DEC-1999 (first entry)  
 XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1048.  
 XX XX  
 XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocytes; CTL; tumour rejection; viral infection; cancer;

KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX WO9945954-A1.  
 XX 16-SEP-1999.  
 XX PD  
 XX PF 13-MAR-1998; 98WO-US005039.  
 XX PR 13-MAR-1998; 98WO-US005039.  
 XX PA (EPIM-) EPIMUNE INC.  
 XX PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;  
 XX WPI, 1999-551214/46.  
 XX DR  
 XX PT New immunogenic peptides with HLA binding motif, useful in treatment and  
 XX diagnosis of cancers and viral diseases.  
 XX PS Claim 1, Page 71, 150pp; English.  
 XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 XX having a human major histocompatibility complex (MHC) Class I (also known  
 XX as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
 XX can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
 XX or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
 XX the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
 XX (CTLs) which destroy antigen-bearing cells are normally induced by an  
 XX antigen in the form of a peptide fragment bound to a HLA molecule, rather  
 XX than the intact foreign antigen itself, and are particularly important in  
 XX tumour rejection and in fighting viral infections. The peptides are  
 XX therefore useful therapeutically to treat or prevent viral infections and  
 XX cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
 XX and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
 XX elicit an immune response in individuals susceptible or otherwise at risk  
 XX of viral infection or cancer, or used to treat chronic or acute  
 XX conditions. They are also useful diagnostically, and can be used to  
 XX induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
 XX the peptide e.g. to produce CTLs ex vivo for infusion back into a  
 XX patient. The polynucleotides encoding the immunogenic peptides are also  
 XX useful therapeutically and for immunisation as above  
 XX  
 XX SQ Sequence 10 AA;  
 XX  
 XX Query Match 90.0%; Score 9; DB 2; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 0.0069;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 2 EYLVPQGGF 10  
 XX |||||  
 XX 1 EYLVPQGGF 9  
 XX DB  
 XX  
 XX RESULT 12  
 XX ADN64633  
 XX ID ADN64633 standard; peptide; 10 AA.  
 XX AC ADN64633;  
 XX XX  
 XX DT 01-JUL-2004 (first entry)  
 XX DE HLA binding peptide #1233.  
 XX XX  
 XX KW cytotoxic; hepatotropic; virucide; anti-inflammatory; anti-HIV;  
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;  
 KW prostate specific antigen; prostate specific membrane antigen;  
 KW hepatitis B virus antigen; hepatitis C virus antigen;  
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;  
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;

KM chondy/loma acuminatum.  
XX  
OS Unidentified.  
XX  
PN WO2004031211-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 03-OCT-2003; 2003WO-US031308.  
XX  
PR 03-OCT-2002; 2002US-0416207P.  
PR 08-OCT-2002; 2002US-0417269P.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sidney J, Southwood S, Sette A;  
XX  
DR WPI; 2004-347953/32.  
XX  
PT New composition of peptides and nucleic acids capable of binding Major  
PT Histocompatibility Complex molecules, useful for diagnosing, preventing  
PT or treating viral infections or cancer, such as prostate cancer,  
PT hepatitis B or AIDS.  
XX  
PS Claim 1; SEQ ID NO 1233; 186bp; English.  
XX  
CC The invention relates to a novel composition comprising one or more  
CC peptides or nucleic acids encoding an HLA binding peptide. The  
CC composition further comprises an HTL epitope. It also comprises a spacer  
CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides  
CC are incorporated as part of a liposome. The peptide is from an antigen  
CC selected from prostate specific antigen (PSA), prostate specific membrane  
CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)  
CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human  
CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),  
CC Papilloma virus, Laesa virus, Mycobacterium tuberculosis (MT), p53,  
CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein  
CC (TKP). The composition is useful for preventing or treating viral  
CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,  
CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondy/loma  
CC acuminatum. The composition is also used for diagnosing such diseases.  
CC This sequence represents a peptide of the invention.  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 90.0%; Score 9; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 BEYLVPQOG 9  
DB 2 BEYLVPQOG 10  
XX  
RESULT 13  
ADP80281  
ID ADP80281 standard; peptide; 10 AA.  
XX  
AC ADP80281;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human HLA-B\*44 epitope vaccine peptide SegID537.  
XX  
KM epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B\*44;  
KM tumour associated antigen peptide; cytosolic; vaccine; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004052917-A2.  
XX  
PD 24-JUN-2004.  
XX

PF 10-DEC-2003; 2003WO-US038949.  
XX  
PR 10-DEC-2002; 2002US-0432017P.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Keogh EA, Southwood S, Flakes JD, Sette A;  
XX  
DR WPI; 2004-468809/44.  
XX  
PT New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,  
PT useful in preparing a composition for diagnosing or treating tumor  
PT associated antigen-related disease.  
XX  
PS Claim 1; SEQ ID NO 537; 244p; English.  
XX  
CC This invention relates to a novel isolated peptide which comprises at  
CC least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given  
CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or  
CC B44 tumour associated antigen peptide. The invention may be useful for  
CC the production of compounds with a cytostatic activity or for the  
CC production of a vaccine. The peptide is useful in preparing a composition  
CC diagnosing or treating tumor associated antigen-related disease. The  
CC present sequence is that of an epitope peptide for use in the peptide of  
CC the invention.  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 90.0%; Score 9; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0069;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 BEYLVPQOG 9  
DB 2 BEYLVPQOG 10  
XX  
RESULT 14  
AAW64460  
ID AAW64460 standard; protein; 9 AA.  
XX  
AC AAW64460;  
XX  
DT 16-OCT-1998 (first entry)  
XX  
DE Human ErbB-2 cytoplasmic domain tyrosine phosphorylated peptide P5.  
XX  
KM Breast; cancer; mack; CSK homologous kinase; CHK; detection; diagnosis;  
KM cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator;  
KM mitogenic signalling; ErbB-2.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Modified-site 4  
FT /note= "phosphorylated tyrosine"  
XX  
PN WO9830704-A1.  
XX  
PD 16-JUL-1998.  
XX  
PF 07-JAN-1998; 98WO-US000420.  
XX  
PR 08-JAN-1997; 97US-0035228P.  
PR 16-JUN-1997; 97US-00876882.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Abraham H, Groopman JE;  
XX  
DR WPI; 1998-399149/34.  
XX

PT Detecting breast cancer by detecting Csk homologous kinase expression -  
PT especially in humans and use of Csk homologous kinase in treatment or  
PT prophylaxis of breast cancer and for producing medicaments.

XX Example 7; Page 33; 54pp; English.

PS AAW6457-M64460 are tyrosine phosphorylated peptides derived from the  
CC cytoplasmic domain of the human ErbB-2/neu receptor. These peptides are  
CC used in a novel method to detect breast cancer using a Csk homologous  
CC kinase (CHK) fragment which is used in a method of detecting cancer in  
CC breast tissue. The method allows diagnosis of breast cancer in mammals,  
CC especially humans. It is based on the discovery that a cytoplasmic  
CC protein tyrosine kinase, CHK, is expressed in human breast tissue, but  
CC not in adjacent tissue. This protein can be used to raise antibodies  
CC which can be included in compositions and diagnostic kits for diagnosis  
CC of breast cancer. The presence of CHK in breast tissue can also be  
CC determined using other standard methods (e.g. Northern blotting) or by  
CC detecting nucleic acid sequences encoding all/a portion of the protein  
CC (e.g. using hybridisation probes). Over-expression of the receptor  
CC tyrosine kinase ErbB-2 has previously been associated with the  
CC development of breast cancer, and CHK specifically interacts with  
CC activated ErbB-2, and may function as a negative regulator of ErbB-2  
CC mediated mitogenic signalling. The compositions may also be used to  
CC design drugs (e.g. which incorporate CHK analogues with greater  
CC biological activity than CHK) and to identify CHK antagonists and  
CC agonists for therapeutic use

XX Sequence 9 AA;

SQ Query Match 60.0%; Score 6; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 BEYLPV 6  
|||||  
DB 2 BEYLPV 7

RESULT 15

AAAG88685  
ID AAG88685 standard; peptide; 9 AA.

XX AAG88685;

AC AAG88685;

XX 11-SEP-2001 (first entry)

DE HER2/NEU DR 3a motif binding peptide core sequence #11.

XX Human, HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytotoxic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

OS Homo sapiens.

OS Synthetic.

OS WO200141787-A1.

OS 14-JUN-2001.

OS 11-DEC-2000; 2000WO-US033591.

OS 10-DEC-1999; 99US-00458299.

OS (EPI-M-) EPI-MUNE INC.

OS Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Celis B;

OS Keogh B;

OS WPI, 2001-374995/39.

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.

PS Disclosure; Page 174; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention

SQ Sequence 9 AA;

Query Match 60.0%; Score 6; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 BEYLPV 6  
|||||  
DB 4 BEYLPV 9

RESULT 16

AAAR41654  
ID AAR41654 standard; peptide; 6 AA.

XX AAR41654;

AC AAR41654;

XX 25-MAR-2003 (revised)

DE 10-MAR-1994 (first entry)

XX Internalisation signal #19.

XX Internalisation signal; core; modulation; receptor; transport; ligand;  
XX cytoplasmic tail; endocytosis.

OS Synthetic.

OS WO9318185-A1.

OS 16-SEP-1993.

OS 01-MAR-1993; 93WO-US001669.

OS 03-MAR-1992; 92US-00844852.

OS (SALK) SALK INST BIOLOGICAL STUDIES.

OS (SCRI) SCRIPS RES INST.

OS Trowbridge IS, Collawn JF, Tainer JA, Kuhn LA;

XX WPI, 1993-303496/38.

XX Modulating receptor mediated transport of ligand into cell - by  
XX introducing heterologous internalisation signal into cell.

XX Claim 19; Page 50; 60pp; English.

PS The sequences given in AAK1636-57 represent the cores of internalisation  
CC signals which were used in the method of the invention for modulating  
CC receptor mediated transport of a ligand into a cell. These sequences are  
CC derived from the cytoplasmic tails of surface receptors. These amino acid  
CC internalisation signals have a tight turn structure. The introduction of  
CC one of these sequences into a receptor within a cell, modulates the  
CC transport of ligand into a cell having a surface receptor reactive with  
CC that ligand. This modulation can cause an increase or a decrease in  
CC endocytosis, depending on the choice of internalisation signal. (Updated  
CC on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 50.0%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 PQQGF 10  
| | | | |  
Db 1 PQQGF 5

RESULT 17

AAE31156  
ID AAE31156 standard; peptide; 9 AA.

XX AAE31156;

XX 24-FEB-2003 (first entry)

XX Human erb2 peptide #41.

XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

XX Homo sapiens.

XX WO200272627-A2.

XX 19-SEP-2002.

XX 11-MAR-2002; 2002MO-BP002666.

XX 09-MAR-2001; 2001US-0274250P.

XX 14-MAY-2001; 2001US-0290353P.

XX 18-MAY-2001; 2001US-0291610P.

XX (CALL-) CALLISTOGEN AG.

XX Wrede P, Walden P, Eichler-Wertens M, Filter M;

XX WPI; 2002-759836/82.

XX Providing, identifying or optimizing peptides for inducing cytotoxic T-  
PT lymphocytes and for treating cancer, comprises selecting conserved  
PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the  
PT protein.

XX Disclosure; Page 8; 32pp; English.

XX The invention relates to a method for providing, identifying or/and  
CC optimising peptides which induce cytotoxic T-lymphocytes and to the uses  
CC of the obtained peptides for vaccination. The method is useful for  
CC providing, identifying and/or optimising peptides that are useful in  
CC manufacturing a pharmaceutical composition for the induction of cytotoxic  
CC T-lymphocytes, and for the prevention, treatment or diagnosis of cancer  
CC or viral infections. The invention is also used in gene therapy. The  
CC present sequence is human erb2 peptide used to illustrate the method of  
CC the invention

XX Sequence 9 AA;

Query Match 50.0%; Score 5; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EBYLV 5  
| | | | |  
Db 5 EBYLV 9

RESULT 18

ADZ50235  
ID ADZ50235 standard; peptide; 9 AA.

XX ADZ50235;

XX 14-JUL-2005 (first entry)

XX Y. pestis cytotoxic T-cell epitope SEQ ID 303.

XX Yersinia pestis infection; antibacterial; infection; epitope; T-cell;  
XX vaccine; biological warfare.

XX Yersinia pestis.

XX WO2005037855-A2.

XX 28-APR-2005.

XX 15-OCT-2004; 2004WO-US033883.

XX 17-OCT-2003; 2003US-0511653P.

XX (PECO-) PECOS LABS INC.

XX Lund O, Lundegaard C, Nielsen M, Worning P, Deans RJ, Buus S;

XX Brunak S;

XX WPI; 2005-315677/32.

XX New cytotoxic Yersinia pestis T-cell epitope comprising 10 amino acids,  
PT useful as a vaccine or diagnostic tool and for inducing immune response  
PT in a subject.

XX Claim 1; SEQ ID NO 303; 235pp; English.

XX The invention relates to a cytotoxic Yersinia pestis T-cell epitope,  
CC selected from any of the 1000 sequences of 9 amino acids appearing as  
CC AD249933-AD250932. Also included are predicting peptides that are  
CC epitopes or can be used as diagnostic tools (comprising predicting which  
CC peptides bind to a HMC molecule (not defined) with high affinity using a  
CC neural network with at least one of the following features: some or all  
CC of the inputs to the neural networks are generated using a hidden Markov  
CC model; or some or all of the inputs are encoded by an amino acid  
CC substitution matrix, different from an identity matrix) and a vaccine or  
CC diagnostic tool using a limited number such as at least 1, 2, 3, 4, 5, 8,  
CC 16, 32, 64, 128, 256, 512 of the peptides of AD249933-AD250932. In  
CC predicting peptides, the prediction of the neural network is combined  
CC with prediction or measurement of one of the following: proteasomal  
CC cleavage sites; MHC binding; presence of sequence or related sequence(s)  
CC in patent databases; YAP binding; gene or protein expression level;  
CC function of the protein; localization of the protein; and similarity to  
CC self proteins. The epitope is useful as a vaccine or diagnostic tool, and  
CC for inducing immune response in a subject (said immunity to Yersinia  
CC pestis infection, the causative agent of plague). The present sequence is  
CC a cytotoxic Yersinia pestis T-cell epitope of the invention.

XX Sequence 9 AA;

Query Match 50.0%; Score 5; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPO 7  
 XX ||||  
 DB 1 YLVPO 5

## RESULT 19

AA61601  
 ID AAR61601 standard; peptide; 10 AA.

XX AAR61601;

XX 25-MAR-2003 (revised)

DT 12-MAY-1995 (first entry)

XX Peptide fragment (1.0757) of c-ERB2 binds HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;  
 KW plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;  
 KW melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;  
 KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;  
 KW 10mer; anchor; human leukocyte antigen.

XX Homo sapiens.

XX MO9420127-A1.

XX 15-SEP-1994.

PF 04-MAR-1994; 94MO-US002353.

XX 05-MAR-1993; 93US-00027146.

PR 04-JUN-1993; 93US-00073205.

PR 29-NOV-1993; 93US-00159184.

XX (CYTE-) CYTEL CORP.

PI Grey HM, Sette A, Sidney J, Kast W;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for

PT treatment or prophylaxis of cancer, virus infection or autoimmune

PT diseases.

XX Example 5; Page 11; 138pp; English.

XX AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1

CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity

CC of at least 1% as compared to a reference peptide (AAR71293). AAR61601

CC has an IC50 of 0.0002 and the sequence occurs at position 1016 in the

CC human c-ERB2 gene product. Peptides of the invention can induce cytotoxic

CC T lymphocytes which can react with target cells. They can be used for the

CC treatment or prophylaxis of cancer, eg prostate cancer or lymphoma, etc.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 10 AA;

QY 1 BEYLV 5

DB 6 BEYLV 10

XX

Query Match 50.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

XX

RESULT 20

AA614919

ID AAB14919 standard; peptide; 10 AA.

XX AAB14919;

XX 11-JAN-2001 (first entry)

DT Random 27-mer library peptide R6-52.

XX RNA-protein fusion; protein library; protein isolation; gene cloning;

XX myc epitope tag.

XX Synthetic.

XX WO200047775-A1.

XX 17-AUG-2000.

PF 01-FEB-2000; 2000MO-US002589.

XX 09-FEB-1999; 99US-00247190.

XX (GENO) GEN HOSPITAL CORP.

XX Szostak JW, Roberts RW, Liu R;

XX WPI; 2000-533022/48.

XX Producing protein or DNA libraries which are useful for improving

PT existing proteins, by in vitro translating protein coding sequences to

PT produce RNA-protein fusions and incubating these protein fusions under

PT high salt conditions.

XX Disclosure; Fig 22; 121pp; English.

XX The present sequence was isolated from an RNA-protein fusion library

CC following selection for peptides that bound to a c-myc monoclonal

CC antibody. RNA-protein fusions comprise a protein covalently linked to the

CC 3' end of its own mRNA. The fusions are made by synthesis and in vitro or

CC in situ translation of an mRNA molecule with a peptide acceptor attached

CC to its 3' end. The RNA-protein fusions are incubated under high salt

CC conditions to produce a protein library. This method is useful for

CC improving or altering existing proteins, as well as for isolating new

CC proteins and nucleic acid or small molecule targets. It may also be used

CC to improve human or humanised single-chain antibodies for the treatment

CC of a number of diseases. The method is useful for the isolation of

CC proteins with specific binding properties, for screening cDNA libraries

CC and cloning new genes on the basis of protein-protein interactions.

CC Unlike prior art, the new method does not rely on maintaining the

CC integrity of an mRNA:ribosome:nascent chain ternary complex, which is

CC very fragile and is therefore of limited use. The method does not rely on

CC topological links between the protein and the nucleic acid so that the

CC information of the protein is retained and can be recovered in readable,

XX nucleic acid form

XX Sequence 10 AA;

QY 1 BEYLV 5

DB 1 BEYLV 5

XX

Query Match 50.0%; Score 5; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

XX

RESULT 21

ADB97832

ID ADE97832 standard; peptide; 10 AA.

XX ADE97832;

XX

AD97832;

XX

12-FEB-2004 (first entry)

XX

Immunogenic HLA-A2.1 binding peptide #314.

XX

cytotoxic; anti-inflammatory; hepatotropic; virucide; anti-HIV;

KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;  
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;  
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;  
 KW immunogenic peptide composition; immune response; prostate cancer;  
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;  
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;  
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;  
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;  
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;  
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;  
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;  
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;  
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;  
 KW human leukocyte antigen A2.1; HLA A2.1;  
 KW immunogenic HLA-A2.1 binding peptide.

XX  
 XX Synthetic.  
 OS  
 XX  
 XX US2003185822-A1.  
 PN  
 XX  
 XX 02-OCT-2003.  
 PD  
 XX  
 XX 03-APR-2002; 2002US-00116557.  
 PF  
 XX  
 XX 05-MAR-1993; 93US-00027146.  
 PR  
 XX 04-JUN-1993; 93US-00073205.  
 PR 29-NOV-1993; 93US-00159184.  
 PR 02-DEC-1994; 94US-00349177.  
 XX  
 XX (GREY/) GREY H M.  
 PA (SETT/) SETTE A.  
 PA (SIDN/) SIDNEY J.  
 PI Grey HM, Sette A, Sidney J;  
 XX  
 XX WPI; 2004-041186/04.  
 DR  
 XX  
 XX Immunogenic peptide composition for preventing, treating or diagnosing  
 PT pathological states, e.g. prostate cancer, hepatitis B and C. Acquired  
 PT immunodeficiency Syndrome, and renal carcinoma, includes conserved  
 PT residues at specified positions.  
 XX  
 XX Example 11; Page 26; 38pp; English.  
 PS  
 XX  
 XX The invention describes an immunogenic peptide composition comprising 9  
 CC residues including a first conserved residue at a second position from N-  
 CC terminus, and a second conserved residue at C-terminal position. The  
 CC inventive peptide composition is used to elicit an immune response  
 CC against a desired antigen for preventing, treating or diagnosing  
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,  
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus  
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune  
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic  
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing  
 CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,  
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,  
 CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic  
 CC purpura, Grave's disease, and Addison's disease. The invention defines  
 CC positions within a motif enabling the selection of the peptides, which  
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the  
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.  
 CC  
 XX  
 XX Sequence 10 AA;  
 SQ

Query Match 50.0%; Score 5; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLV 5  
 DB 6 EBYLV 10

RESULT 22  
 AAR23688  
 ID AAR23688 standard; protein; 6 AA.  
 XX  
 XX AAR23688;  
 AC  
 XX  
 XX 03-NOV-1992 (first entry)  
 DT  
 XX  
 XX Cyclic hirudin derivative #20.  
 DE  
 XX  
 XX Blood clotting; platelet aggregation; inhibition; atherosclerosis;  
 KW myocardial infarction; pulmonary embolism; acute venous thrombosis;  
 KW arterial embolism; medicinal leech; cyclic.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FH 1  
 FT Modified-site /label= Orn  
 FT /note= "alpha-amino group forms peptide linkage with  
 FT Leu(6) "  
 FT Modified-site 6 /note= "forms peptide linkage with Orn(1) "  
 FT  
 XX  
 XX EP482966-A.  
 PN  
 XX  
 XX 29-APR-1992.  
 PD  
 XX  
 XX 18-SEP-1991; 91EP-00402471.  
 PF  
 XX  
 XX 26-SEP-1990; 90FR-00011842.  
 PR  
 XX  
 XX (ADIR ) ADIR & CIE.  
 PA  
 XX  
 XX Fauchere JL, Thuireau C, Picard I, Verbeuren T;  
 PI  
 XX  
 XX WPI; 1992-143016/18.  
 DR  
 XX  
 XX New hirudin derivs. with non natural peptide features - are powerful, non  
 PT -haemorrhagic anticoagulants, etc., stable against proteolysis.  
 PT  
 XX  
 XX Example 16; Page 10; 27pp; French.  
 PS  
 XX  
 XX This peptide is one specific example of a highly generic formula for  
 CC hirudin derivatives. The derivs. are anticoagulant, antithrombotic and  
 CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic  
 CC action and show anticoagulant activity at doses 10 times lower than known  
 CC hirudin derivs. The derivs. are also stable against proteolysis  
 CC  
 XX  
 XX Sequence 6 AA;  
 SQ

Query Match 40.0%; Score 4; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
 DB 3 EBYL 6

RESULT 23  
 AAR23682  
 ID AAR23682 standard; protein; 6 AA.  
 XX  
 XX AAR23682;  
 AC  
 XX  
 XX 03-NOV-1992 (first entry)  
 DT  
 XX  
 XX Cyclic hirudin derivative #14.  
 DE  
 XX  
 XX Blood clotting; platelet aggregation; inhibition; atherosclerosis;  
 KW myocardial infarction; pulmonary embolism; acute venous thrombosis;



KW arterial embolism; medicinal leech; cyclic.  
 XX Synthetic.  
 XX Key  
 XX Modified-site 1 Location/Qualifiers  
 PT /label= Orn  
 PT /note= "side-chain amino group forms peptide linkage with  
 Leu(6)"  
 PT Modified-site 6  
 PT /note= "forms peptide linkage with Orn(1)"  
 PN EP482966-A.  
 XX 29-APR-1992.  
 XX 18-SEP-1991; 91EP-00402471.  
 XX 26-SEP-1990; 90FR-00011842.  
 XX (ADIR ) ADIR & CIR.  
 PI Fauchere JL, Thurielau C, Picard I, Verbeuren T;  
 XX WPI; 1992-143016/18.  
 XX New hirudin derivs. with non natural peptide features - are powerful, non  
 PT -haemorrhagic anticoagulants, etc., stable against proteolysis.  
 XX Example 10; Page 9; 27pp; French.  
 CC This peptide is one specific example of a highly generic formula for  
 CC hirudin derivatives. The derivs. are anticoagulant, antithrombotic and  
 CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic  
 CC action and show anticoagulant activity at doses 10 times lower than known  
 CC hirudin derivs. The derivs. are also stable against proteolysis  
 XX  
 SQ Sequence 6 AA;  
 Query Match 40.0%; Score 4; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EHYL 4  
 DB 3 EHYL 6  
 RESULT 24  
 AAY24186  
 ID AAY24186 standard; peptide; 6 AA.  
 XX  
 AC AAY24186;  
 XX  
 DT 10-SEP-1999 (first entry)  
 XX  
 DE Human pepsinogen II and pepsin II assaying peptide #19.  
 XX  
 KM Human; pepsinogen II; pepsin II; diagnosis; gastropathy; gastric cancer;  
 KM gastric ulcer.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PH Key  
 PT Modified-site 5 Location/Qualifiers  
 PT /note= "2-naphthylalanine"  
 PT Modified-site 6  
 PT /note= "modified C-terminal: Ala-pMA"  
 XX  
 PN MO9932511-A1.  
 XX  
 PD 01-JUL-1999.

XX 21-DEC-1998; 98WO-JP005780.  
 PF  
 XX 22-DEC-1997; 97JP-00364796.  
 PR  
 PR 13-JUL-1998; 98JP-00215113.  
 XX  
 PA (ONOY ) ONO PHARM CO LTD.  
 XX  
 PI Hayashi A, Matsuo M;  
 XX WPI; 1999-405156/34.  
 XX  
 PT New peptide substitutes useful in the diagnosis of gastric ulcers.  
 XX  
 PS Claim 5; Page 44; 56pp; English.  
 CC AAY24168 to AAY24238 represents peptide (1) substitutes specific for  
 CC human pepsin II. (1) may be used for assaying human pepsin II or human  
 CC pepsinogen II useful in the diagnosis of gastropathies such as gastric  
 CC cancer or gastric ulcer  
 XX  
 SQ Sequence 6 AA;  
 Query Match 40.0%; Score 4; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 P00G 9  
 DB 1 P00G 4  
 RESULT 25  
 AAU80407  
 ID AAU80407 standard; peptide; 6 AA.  
 XX  
 AC AAU80407;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Positive cell selection associated peptide #4.  
 XX  
 KM Positive cell selection; cancer; immunosuppression; gene therapy;  
 KM breast cancer; prostate cancer; colon cancer; lung cancer; lymphoma;  
 KM myeloma; melanoma; leukaemia; ovarian cancer; pancreatic cancer;  
 KM adrenal cancer; renal cancer; cell carcinoma; cervical cancer;  
 KM hepatic cancer; stomach cancer; neuroblastoma; stem cell;  
 KM cell-related disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200190153-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PE 23-MAY-2001; 2001WO-US016840.  
 XX  
 PR 23-MAY-2000; 2000US-00578784.  
 PR 11-SEP-2000; 2000US-00659469.  
 XX  
 PA (NEXB-) NEXEL THERAPEUTICS INC.  
 XX  
 PI Schaeffer AT, Tseng-Law J, Thornton JR, Van Epps DB;  
 XX WPI; 2002-089920/12.  
 XX  
 PT New peptide-ligand conjugates, useful as reagents for cell selection,  
 PT particularly for positively isolating stem cells, which are useful for  
 PT transplantation, especially for treating a condition such cancer or  
 PT immunosuppression.  
 XX  
 PS Disclosure; Page 15; 116pp; English.  
 XX

CC The invention describes a peptide-ligand conjugate comprising a peptide  
 CC conjugated to a first ligand, where a free form of the peptide is capable  
 CC of displacing a second ligand specific for the peptide. The peptide-  
 CC ligand conjugate is useful as reagents for cell selection, particularly  
 CC for positively selecting cells from a population. The peptide-ligand  
 CC conjugate is particularly useful for isolating stem cells. Isolation of  
 CC rare cell types to high purity has important applications in molecular  
 CC medicine. Diagnosis of cell-related disease requires methods for  
 CC detection. Isolation and analysis of individual cells, even if the cells  
 CC are rare. The cells are useful in cell-based therapies in gene therapy  
 CC applications. The isolated stem cells are also useful for  
 CC transplantation, especially for treating a condition such as cancer (e.g.,  
 CC breast, prostate, colon, lung, lymphoma, myeloma, melanoma, leukemia,  
 CC ovarian, pancreatic, adrenal, renal, cell carcinoma, cervical, hepatic,  
 CC stomach and neuroblastoma) or immunosuppression. This sequence is one of  
 CC 57 peptides (AAU80440-AAU80460) capable of displacing a ligand specific  
 CC for the peptide and used to form target specific peptide-ligand  
 CC conjugates, used in the cell selection methods described in the invention  
 CC  
 CC Sequence 6 AA,  
 CC  
 CC

Query Match	40.0%;	Score 4;	DB 5;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 2e+06;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	7	QQGF	10
Db	1	QQGF	4

RESULT 26  
AAR23680  
ID AAR23680 standard; protein; 7 AA.

AC AAR23680;

DT 03-NOV-1992 (first entry)

Cyclic hydridin derivative #12.

KW Blood clotting; platelet aggregation; inhibition; atherosclerosis;  
 KW myocardial infarction; pulmonary embolism; acute venous thrombosis  
 KW arterial embolism; medicinal leech; cyclic.

OS Synthetic.

FH	Key	Location/Qualifiers
FT	Modified-site	2

PT	/note="side-chain amino group forms peptide linkage with
PT	Leu(7)"
Modified-site	
PT	7

PN EP482966-A.

PD 29-APR-1992.

PF 18-SEP-1991; 91EP-00402471.

PR 26-SEP-1990; 90FR-00011842.

PA (ADIR ) ADIR &amp; CIE.

PI Fauchere JL, Thuriere C, Picard I, Verbeuren T,

DR WPI; 1992-143016/18.

PT New hirudin derivs. with non natural peptide features - are powerful, non  
PT -haemorrhagic anticoagulants, etc., stable against proteolysis.

PS Example 8; Page 8; 27pp; French.

CC This peptide is one specific example of a highly generic formula for  
CC hirudin derivatives. The derivs. are anticoagulant, antithrombotic and  
CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic  
CC action and show anticoagulant activity at doses 10 times lower than known  
CC hirudin derivs. . The derivs. are also stable against proteolysis  
XX  
SQ Sequence 7 Aa;

Query Match	40.0%	Score 4	DB 2	Length 7
Best Local Similarity	100.0%	Pred. No.	2e+06	
Matches	4	Conservative	0	Indels 0
		Mismatches	0	Gaps 0

QY	1	EEYL	4
Db	4	EEYL	7

RESULT 27  
AAR23681  
ID AAR23681 standard; protein; 7 AA

AC AAR23681;  
VV

DT 03-NOV-1992 (first entry)

Cyclic hirudin derivative #13.

KM Blood clotting; platelet aggregation; inhibition; atherosclerosis;  
KM myocardial infarction; pulmonary embolism; acute venous thrombosis;  
KM arterial embolism; medicinal leech; cyclic.

OS Synthetic.

FH	Key	Location/Qualifiers
FT	Modified-site	1

Modified-site	2	/label= Orn	/note= "side-chain amino group forms peptide linkage with
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**FT Modified-site**

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PA (ANDP ) ANDP & CTR

**XX**      **Eau Claire**

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DR  
XX  
WPI, 1992-143016/18.

PT	-haemorrhagic anticoagulants, et
XX	
PS	Example 9; Page 9; 27pp; French.

CC This peptide is one specific example of a highly generic formula for  
CC hindin derivatives. The derivs. are anticoagulant, antithrombotic and  
CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic  
CC action and show anticoagulant activity at doses 10 times lower than known  
CC hindin derivs. . The derivs. are also stable against proteolysis

**SQ Sequence 7 AA;**

Query Match	40.0%	Score 4	DB 2	Length 7
Best Local Similarity	100.0%	Pred. No.	2e+06	
Matches 4	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy 1 BEYL 4  
 ||||  
 Db 4 BEYL 7

# RESULT 28

AAR91861  
 ID AAR91861 standard; peptide; 7 AA.

AC AAR91861;

DT 28-NOV-1996 (first entry)

DE Reversible thrombin inhibitor for coating intravascular medical devices.

KM Anti-thrombotic; blood clot; prevention; intravascular; coating;

KW medical equipment; surgical; dialysis; blood oxygenator; catheter;

XX plasmapheresis.

OS Synthetic.

PN WO961668-A1.

PD 25-APR-1996.

PF 13-OCT-1995; 95WO-US013171.

PR 17-OCT-1994; 94US-00324413.

PA (SURF-) SURFACE GENESIS INC.

PI Subramaniam R;

DR WPI; 1996-221729/22.

PT Mfr. of medical device with biocompatible coating - by providing surface

PT with first reactive group contacted with agent reactive with first gp.

PT for covalent binding.

PS Claim 9; Page 13; 29pp; English.

CC AAR91861 is a reversible inhibitor of thrombosis. The peptide was

CC covalently bonded to a surface for coating medical equipment for the

CC prevention of thrombogenesis. Equipment in which this is useful includes

CC intravascular catheters, blood oxygenators, dialysis and plasmapheresis

CC machines. Also disclosed in the specification are uses of promoters of

CC thrombosis in the same way which are useful to coat bandages, sutures,

CC etc. to promote wound healing

CC Sequence 7 AA;

SO Query Match 40.0%; Score 4; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 BEYL 4

||||

Db 3 BEYL 6

# RESULT 29

AAM59316  
 ID AAM59316 standard; peptide; 7 AA.

AC AAM59316;

DT 24-SEP-1998 (first entry)

DE Non-polio enterovirus peptide fragment 40A.

KM Non-polio enterovirus; NPEV; enteroviral disease; aseptic meningitis;

KW vaccination.

XX Enterovirus sp.

OS MO9814611-A2.

PN 09-APR-1998.

PD 01-OCT-1997; 97WO-US017734.

PF 02-OCT-1996; 96US-0027353P.

PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Kilpatrick D;

PI WPI; 1998-240106/21.

DR Identifying non-polio enteroviruses - using primers which hybridise to

PT sense and antisense strands that encode conserved non-polio enterovirus

PT peptide sequences.

PS Claim 4; Page 23; 47pp; English.

PN The peptide sequences AAM59298-W59344 are amplified by primers to detect

CC the presence of a non-polio enterovirus (NPEV) in a sample. The primers

CC and assays are used to detect NPEVs in a sample, to serotype these

CC viruses, to diagnose enteroviral diseases and medical conditions, and to

CC correlate (or disprove a correlation between) specific symptoms or

CC combinations of symptoms with the presence of a particular enterovirus.

CC They can be used for diseases such as aseptic meningitis. The detection

CC of NPEV infections and their correlation with medical conditions will

CC make possible vaccines and methods of treatment

CC Sequence 7 AA;

SO Query Match 40.0%; Score 4; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LVPQ 7

||||

Db 4 LVPQ 7

# RESULT 30

AAY50074  
 ID AAY50074 standard; peptide; 7 AA.

AC AAY50074;

DT 19-JAN-2000 (first entry)

DE Coxsackievirus A VP1 conserved epitope 40.

KM Virus; epitope; target; degenerate; PCR; primer; amplification; VP1;

KW nonstructural protein 2A; conserved; base analogue; inosine;

KM predetermined nucleotide; diagnosis; enterovirus; poliovirus.

OS Synthetic.

OS Coxsackievirus.

PN WO9953097-A2.

PD 21-OCT-1999.

PF 06-APR-1999; 99WO-US007513.

PR 15-APR-1998; 98US-0081944P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Kilpatrick DR;

XX

DR WPI; 1999-620444/53.  
DR N-PSDB; AAZ30993.

PT Designing degenerate polymerase chain reaction primers.

PS Example 3; Page 18; 30pp; English.

XX This sequence represents a conserved Coxsackievirus A (serotype A16) VP1  
CC epitope. The invention relates to a novel method for designing degenerate  
CC PCR primers (AAZ30975-231000, AAZ32601- AAZ32611) for amplifying target  
CC polynucleotides. This method comprises identifying uniquely conserved  
CC amino acid sequences (e.g., this epitope) in target proteins; synthesizing  
CC degenerate polynucleotides encoding the conserved sequences; and  
CC substituting the synthesised polynucleotides with up to four  
CC predetermined nucleotides (e.g., inosine) at degenerate nucleotide  
CC positions. The nucleic acids comprise no more than 7 degenerate  
CC positions, have no more than 2 adjacent predetermined nucleotides and the  
CC predetermined nucleotides are 3 bases away from the 3' end of the  
CC synthesised strand. The degenerate primers are useful for amplifying  
CC target polynucleotides by the polymerase chain reaction (PCR). The use of  
CC the method of designing degenerate primers useful for the detection of  
CC polioviruses in clinical samples is described in US585477. The degenerate  
CC primers facilitate PCR amplification of unknown polynucleotides, where  
CC the amino acid sequence encoded is known. The primers also allow for the  
CC correlation of the subsequent molecular based diagnosis with a  
CC serologically derived diagnosis

XX Sequence 7 AA;

Query Match 40.0%; Score 4; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LVPO 7  
|||  
4 LVPO 7

DB 4 LVPO 7

RESULT 31

AAV24181  
ID AAV24181 standard; peptide; 7 AA.

XX AAV24181;

XX 10-SEP-1999 (first entry)

XX Human pepsinogen II and pepsin II assaying peptide #14.

XX Human; pepsinogen II; pepsin II; diagnosis; gastrophpy; gastric cancer;

XX gastric ulcer.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 6 /note= "4-iodo-phenylalanine"

XX Modified-site 7 /note= "modified C-terminal: Ala-pNa"

XX WO9932511-A1.

XX 01-JUL-1999.

XX 21-DEC-1998; 98WO-JP005780.

XX 22-DEC-1997; 97JP-00364796.

XX 13-JUL-1998; 98JP-00213513.

XX (ONOV ) ONO PHARM CO LTD.

XX Hayashi A, Matsuo M;

XX

DR WPI; 1999-405156/34.

XX New peptide substitutes useful in the diagnosis of gastric ulcers.

XX Claim 5; Page 43; 56pp; English.

XX AAZ24168 to AAV24238 represents peptide (I) substitutes specific for  
CC human pepsin II. (I) may be used for assaying human pepsin II or human  
CC pepsinogen II useful in the diagnosis of gastropathies such as gastric  
CC cancer or gastric ulcer

XX Sequence 7 AA;

Query Match 40.0%; Score 4; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VPOQ 8  
|||  
1 VPOQ 4

DB 1 VPOQ 4

RESULT 32

AAK23690  
ID AAK23690 standard; protein; 8 AA.

XX AAK23690;

XX 03-NOV-1992 (first entry)

XX Cyclic hirudin derivative #22.

XX Blood clotting; platelet aggregation; inhibition; atherosclerosis;

XX myocardial infarction; pulmonary embolism; acute venous thrombosis;

XX arterial embolism; medicinal leech; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /label= OTHER

XX Modified-site 3 /note= "pyroglutamic acid"

XX Modified-site 3 /label= Orn

XX Modified-site 8 /note= "side-chain amino group forms peptide linkage with  
Leu(8) "

XX Modified-site 8 /note= "forms peptide linkage with Orn(3) "

XX EP482966-A.

XX 29-APR-1992.

XX 18-SEP-1991; 91EP-00402471.

XX 26-SEP-1990; 90FR-00011842.

XX (ADIR ) ADIR & CIE.

XX Fauchere JL, Thurieu C, Picard I, Verbeuren T;

XX WPI; 1992-143016/18.

XX New hirudin derivs. with non natural peptide features - are powerful, non

XX -haemorrhagic anticoagulants, etc., stable against proteolysis.

XX Example 18; Page 10; 27pp; French.

XX This peptide is one specific example of a highly generic formula for  
CC hirudin derivatives. The derivs. are anticoagulant, antithrombotic and  
CC platelet-aggregation inhibiting agents. The derivs. have no haemorrhagic  
CC action and show anticoagulant activity at doses 10 times lower than known  
CC hirudin derivs. The derivs. are also stable against proteolysis

XX Sequence 8 AA;

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
5 EBYL 8

RESULT 33

AAW23691  
ID AAW23691 standard; protein; 8 AA.

AC AAW23691;

DT 03-NOV-1992 (first entry)

XX Cyclic hirudin derivative #23.

XX Blood clotting; platelet aggregation; inhibition; atherosclerosis;

KW myocardial infarction; pulmonary embolism; acute venous thrombosis;

KW arterial embolism; medicinal leech; cyclic.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT Modified-site 3 /note= "3-((3-hydroxy-4-methoxycarbonyl)phenyl) carbamoylmethylcarbamoyl(propionyl)"

FT Modified-site 8 /note= "side-chain amino group forms peptide linkage with Leu(8)"

FT Modified-site 8 /note= "forms peptide linkage with Orn(3)"

PN EP482966-A.

PD 29-APR-1992.

PF 18-SEP-1991; 91EP-00402471.

PR 26-SEP-1990; 90FR-00011842.

PA (ADIR ) ADIR & CIE.

PI Fauchere JL, Thurleau C, Picard I, Verbeuren T;

DR WPI; 1992-143016/18.

XX New hirudin derive, with non natural peptide features - are powerful, non

PT -haemorrhagic anticoagulants, etc., stable against proteolysis.

PS Example 19; Page 10; 27pp; French.

XX This peptide is one specific example of a highly generic formula for

CC hirudin derivatives. The derives, are anticoagulant, antithrombotic and

CC platelet-aggregation inhibiting agents. The derives, have no haemorrhagic

CC action and show anticoagulant activity at doses 10 times lower than known

CC hirudin derives. The derives, are also stable against proteolysis

XX Sequence 8 AA;

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||

DB 5 EBYL 8

RESULT 34

AAW21534  
ID AAW21534 standard; peptide; 8 AA.

AC AAW21534;

DT 02-AUG-1999 (first entry)

XX Hirudin peptide 2 (residues 57-64).

KW Platelet aggregation; hirudin; inhibitor; coagulation; leech;

KW heparin-induced thrombocytopenia.

OS Hirudo medicinalis.

PN US5256559-A.

PD 26-OCT-1993.

XX 27-MAR-1991; 91US-00677609.

PR 04-MAR-1988; 88US-00164178.

PR 29-SEP-1988; 88US-00251150.

PR 05-DEC-1988; 88US-00280618.

PR 28-FEB-1989; 89US-00314755.

XX (BIOJ ) BIOGEN INC.

PA (UYBO-) UNIV BOSTON.

PI Maraganore JM, Jakubowski JA;

DR WPI; 1993-350828/44.

XX Platelet aggregation inhibition in vitro and in vivo - using specified

PT hirudin peptide(s).

PS Example; Fig 2; 22pp; English.

XX The invention relates to a method for inhibiting platelet aggregation in

CC stored platelets. The method comprises storing platelets in the presence

CC of a composition comprising a peptide and a carrier, where the peptide is

CC of formula Y-Phe-Glu-Glu-Ile-Pro-Glu-Glu-X-Z or Asn-Gly-Asp-Phe-Glu-Glu-

CC Ile-Pro-Glu-Glu-Tyr-Z, Y = H, an amino protecting group, Asp or sequence

CC of at least two C-terminal amino acids from the sequence Val-Thr-Gly-Glu-

CC Gly-Thr-Pro-Lys-Pro-Gln-Ser-His-Asn-Asp-Gly-Asp; Z = OH, Leu or Leu-Gln; X =

CC Tyr with a negatively charged side gp. The peptides are derived from

CC hirudin, a natural inhibitor of coagulation, produced by the blood

CC sucking leech Hirudo medicinalis. The peptides may be used to treat

CC patients who are suffering from or have suffered from heparin-induced

CC thrombocytopenia

XX Sequence 8 AA;

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
5 EBYL 8

RESULT 35

AAW29068  
ID AAW29068 standard; peptide; 8 AA.

AC AAW29068;

DT 25-MAR-2003 (revised)

DT 17-MAR-1998 (first entry)  
 XX Peptide fragment of new thrombin inhibitor compound.  
 DE  
 XX alpha-ketoamide linkage; thrombin inhibitor; hirudin; thrombus.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 7  
 FT /note= "optionally iodinated as Tyr(3-iodo) or Tyr(3,5-  
 FT diiodo)"  
 FT Modified-site 8  
 FT /note= "optionally in the form of a C-terminal amide"  
 XX  
 XX US5670479-A.  
 PN 23-SEP-1997.  
 XX  
 XX 25-MAR-1994; 94US-00218329.  
 PP  
 XX 25-MAR-1993; 93US-00037574.  
 PR  
 XX (CORV-) CORVAS INT INC.  
 PA  
 XX Webb TR, Vlaeuk GP, Abelman MM, Pearson DA;  
 PI WPI; 1997-479505/44.  
 DR  
 XX New peptide alpha-keto:amide analogues - useful as thrombin inhibitors  
 XX for therapy and diagnosis of thrombosis.  
 PT  
 XX  
 XX Claim 1; Col 196, 197; 116pp; English.  
 PS  
 XX The patent describes new thrombin inhibitor peptides consisting of an N-  
 CC protected Asp-Pro-Arg (or analogue) tripeptide joined via an alpha-  
 CC ketoamide linkage (-CO-CO-NH-) to a spacer peptide (preferably (Gly)5) in  
 CC turn joined to a peptide which is homologous to amino acids 53-64 of  
 CC hirudin. The peptides are effective at low doses for preventing or  
 CC treating thrombus formation. The present sequence is a preferred fragment  
 CC of the new peptides, consisting of a portion of the hirudin homologue.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC  
 SQ Sequence 8 AA;  
 Query Match 40.0%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 1 EHYL 4  
 ||||  
 DB 5 EHYL 8  
 RESULT 36  
 AAY55243  
 ID AAY55243 standard; peptide; 8 AA.  
 AC AAY55243;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 XX ATCC HB 11646 monoclonal antibody 9069 releasing peptide SEQ ID NO:137.  
 DE  
 XX Antibody releasing peptide; CD34; hybridoma; binding; antigen;  
 KW cell surface antigen; identification; haematopoietic stem cell; tumour;  
 KW cancer; immune system; therapy; displacement.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 XX US5968753-A.  
 PN  
 XX

PD 19-OCT-1999.  
 XX  
 XX 07-JUN-1995; 95US-00482228.  
 PP  
 XX 14-JUN-1994; 94US-00259427.  
 PR  
 XX (NEXE-) NEXELL THERAPEUTICS INC.  
 PA  
 XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;  
 PI Al-Abdaly FA;  
 DR WPI; 1999-590399/50.  
 XX  
 XX Short peptides useful for displacing antibodies from cell surface  
 PT antigens.  
 PT  
 XX  
 XX Example 8; Col 27; 81pp; English.  
 PS  
 XX The present invention describes peptides of 4-17 amino acids which  
 CC displace either the anti-CD34 monoclonal antibody designated 561, the  
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC HB-  
 CC 11646 (designated 9069), the anti-CD34 antibody produced by hybridoma  
 CC ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced  
 CC by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a  
 CC target cell. The peptides are useful for displacing antibodies bound to  
 CC cell surfaces to release cells that have been positively selected by  
 CC antibody-mediated binding to beads or other solid support. AAY5107 to  
 CC AAY5319 represent peptides used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 8 AA;  
 Query Match 40.0%; Score 4; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 7 QGGF 10  
 ||||  
 DB 1 QGGF 4  
 RESULT 37  
 AAY86989  
 ID AAY86989 standard; peptide; 8 AA.  
 AC AAY86989;  
 XX  
 DT 09-MAY-2000 (first entry)  
 XX  
 XX Human haematopoietic CD34+ cell binding peptide SEQ ID #137.  
 DE  
 XX Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;  
 KW non-enzymatic cell selection method; haematopoietic stem cell;  
 KW haematopoietic progenitor cell; antibody 561; breast cancer cell;  
 KW antibody 9187; cell surface determinant; diagnostic cell based assay.  
 XX  
 OS Homo sapiens.  
 OS  
 XX US6017719-A.  
 PN 25-JAN-2000.  
 XX  
 XX 07-JUN-1995; 95US-00482528.  
 PP  
 XX 14-JUN-1994; 94US-00259427.  
 PR  
 XX (NEXE-) NEXELL THERAPEUTICS INC.  
 PA  
 XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;  
 PI Al-Abdaly FA;  
 DR WPI; 2000-136676/12.  
 XX

PT Non-enzymatic method for the positive selection of target cells from a  
 PT heterogeneous cell suspension, useful for selecting human breast cancer  
 PT cells from a patient's blood or bone marrow.

PS Example 8; Col 32; 82pp; English.

CC This sequence represents a human haematopoietic CD34+ cell binding  
 CC peptide, and was used to test the method of the invention. The method is  
 CC a non-enzymatic method for the positive selection of one or more target  
 CC cells from a heterogeneous cell suspension, by using specific peptides  
 CC which effect the displacement and release of a specific target cell from  
 CC a specific monoclonal antibody. The method is useful for positive  
 CC selection and specific release of target human haematopoietic  
 CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and  
 CC the antibody 561. The method is also useful for positive selection and  
 CC specific release of target human breast cancer cells, bound by the  
 CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or  
 CC bone marrow. Identification of peptide epitopes for antibodies which  
 CC recognise cell surface determinants also allows construction of  
 CC diagnostic cell based assays. The peptide mediated release is enzyme free  
 CC and thus leaves the cell surface proteins intact. Moreover, peptide  
 CC mediated release leaves the target cell free of bound antibody or  
 CC antibody fragments. The method also produces a high yield of functional  
 CC target cells and is relatively inexpensive to carry out

SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 OQGF 10  
 ||||  
 1 OQGF 4

DB

RESULT 39  
 AAB82748  
 ID AAB82748 standard; peptide; 8 AA.

AC AAB82748;

DT 29-OCT-2001 (first entry)

DE Wheat glutenin repeat peptide variant.

KW Tyrosine; di-tyrosine bond; crosslinking; glutenin; viscoelasticity;  
 wheat; grain; dough; baking; mutant; mutein.

OS Triticum aestivum.  
 OS Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 4 /note= "Tyr in native peptide"

FT WO200154486-A1.

PN 02-AUG-2001.

PD 27-JAN-2000; 2000MO-US002106.

PF 26-JAN-2000; 2000US-00491259.

PR (UNITV ) UNITV KANSAS STATE RES FOUND.

PA Tilley K;

PI WPI; 2001-536416/59.

DR N-PSDB; AAH26439.

PT Polymeric structure comprising a pair of discrete bio- or synthetic  
 PT polymers coupled together via a tyrosine bond, useful when the polymer is

PT a plant (e.g. wheat) protein that can be used to, for e.g. modify  
 PT physical properties of dough.

PS Example 32; Page 48; 104pp; English.

CC The present sequence is that of a variant of a conserved repeat peptide  
 CC pair of wheat glutenin, and does not include the peptide-bonded tyrosine  
 CC residue with Phe. Oligonucleotides (see AAH26436-45) coding for the  
 CC native repeat and its variants (see AAB82746-54) were expressed in  
 CC glutenin proteins in order to analyse the effect of the precise repeat  
 CC amino acid sequence on di-tyrosine formation in doughs. The proteins were  
 CC produced in *Escherichia coli*, purified and added to flour to test the  
 CC effect of mutations on product quality. The proteins were also produced  
 CC in transformed wheat plants. The invention is based on the discovery that  
 CC a class of tyrosine-containing peptides, such as the glutenin repeat  
 CC peptide, form tyrosine bonds in the protein fraction of wheat, wheat  
 CC flour, wheat dough and its product. These tyrosine bonds have a profound  
 CC and previously unrecognized effect on product quality. This discovery  
 CC allows effective genetic manipulation of wheat and other grains in order  
 CC to control tyrosine bond levels in the grain protein. It also leads to  
 CC methods for monitoring and/or altering tyrosine bond levels during plant  
 CC growth, flour manufacture and dough formation and processing

SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 OQGF 10  
 ||||  
 1 OQGF 4

DB

RESULT 39  
 AAB82746  
 ID AAB82746 standard; peptide; 8 AA.

AC AAB82746;

DT 29-OCT-2001 (first entry)

DE Wheat glutenin repeat peptide variant.

KW Tyrosine; di-tyrosine bond; crosslinking; glutenin; viscoelasticity;  
 wheat; grain; dough; baking; mutant; mutein.

OS Triticum aestivum.  
 OS Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 4 /note= "Tyr in native peptide"  
 FT Misc-difference 5 /note= "Tyr in native peptide"

FT WO200154486-A1.

PN 02-AUG-2001.

PD 27-JAN-2000; 2000MO-US002106.

PF 26-JAN-2000; 2000US-00491259.

PR (UNITV ) UNITV KANSAS STATE RES FOUND.

PA Tilley K;

PI WPI; 2001-536416/59.

DR N-PSDB; AAH26437.

PT Polymeric structure comprising a pair of discrete bio- or synthetic





```
ID ADK37330 standard; peptide; 8 AA.
XX
XX ADK37330;
AC
XX 06-MAY-2004 (first entry)
DT
XX Hepatitis B virus (HBV) epitope #198.
DE
XX HBV, cytotoxic T-cell response; immunogenic activity;
KM human leukocyte antigen; HLA; HBV infection; HBV epitope;
KW antiinflammatory; hepatotropic; virucide.
XX
XX Hepatitis B virus.
OS
XX US6689363-B1.
PN
XX 10-FEB-2004.
PD
XX 27-JAN-1999; 99US-00239043.
PF
XX 29-JAN-1992; 92US-00827682.
XX 27-APR-1992; 92US-00874491.
PR 07-AUG-1992; 92US-00926666.
PR 26-AUG-1992; 92US-00935811.
PR 05-MAR-1993; 93US-00027146.
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 06-AUG-1993; 93US-00103396.
PR 16-FEB-1994; 94US-00197484.
PR 04-MAR-1994; 94US-00205713.
PR 23-NOV-1994; 94US-00344824.
PR 01-DEC-1994; 94US-00347610.
PR 13-MAR-1996; 96US-0013363P.
PR 12-MAR-1997; 97US-00820360.
PR 25-NOV-1997; 97US-00978291.
PR 10-NOV-1998; 98US-00189702.
XX
XX (EPTM-) EPTMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Vitello MA, Livingston BD;
PI Cells E, Kubo RT, Grey HM, Chesnut RW;
PI
XX WPI; 2004-141419/14.
DR
XX Hepatitis B virus (HBV) vaccine composition useful for inducing cellular
PT immune responses to HBV or for preventing and treating HBV infection.
PS
XX Disclosure; SEQ ID NO 198; 73pp; English.
XX
XX The invention relates to a hepatitis B virus (HBV) vaccine composition
CC comprising a pharmaceutical carrier and an isolated peptide less than 25
CC or less than 15 amino acids in length. The invention also relates to a
CC method of inducing a cytotoxic T-cell response to HBV in a mammal and a
CC method of monitoring immunogenic activity of the vaccine in a patient
CC having a known human leukocyte antigen (HLA) type. The composition and
CC methods are useful for preventing and treating HBV infection. This
CC sequence represents an HBV epitope used in the scope of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 8 AA:
SQ
Query Match 40.0%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EYLV 5
DB 5 EYLV 8
RESULT 43
```

```
ADK38478
ID ADK38478 standard; peptide; 8 AA.
XX
XX ADK38478;
AC
XX 06-MAY-2004 (first entry)
DT
XX Hepatitis B virus (HBV) epitope #1346.
DE
XX HBV, cytotoxic T-cell response; immunogenic activity;
KM human leukocyte antigen; HLA; HBV infection; HBV epitope;
KW antiinflammatory; hepatotropic; virucide.
XX
XX Hepatitis B virus.
OS
XX US6689363-B1.
PN
XX 10-FEB-2004.
PD
XX 27-JAN-1999; 99US-00239043.
PF
XX 29-JAN-1992; 92US-00827682.
XX 27-APR-1992; 92US-00874491.
PR 07-AUG-1992; 92US-00926666.
PR 26-AUG-1992; 92US-00935811.
PR 05-MAR-1993; 93US-00027146.
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 06-AUG-1993; 93US-00103396.
PR 16-FEB-1994; 94US-00197484.
PR 04-MAR-1994; 94US-00205713.
PR 23-NOV-1994; 94US-00344824.
PR 01-DEC-1994; 94US-00347610.
PR 13-MAR-1996; 96US-0013363P.
PR 12-MAR-1997; 97US-00820360.
PR 25-NOV-1997; 97US-00978291.
PR 10-NOV-1998; 98US-00189702.
XX
XX (EPTM-) EPTMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Vitello MA, Livingston BD;
PI Cells E, Kubo RT, Grey HM, Chesnut RW;
PI
XX WPI; 2004-141419/14.
DR
XX Hepatitis B virus (HBV) vaccine composition useful for inducing cellular
PT immune responses to HBV or for preventing and treating HBV infection.
PS
XX Disclosure; SEQ ID NO 1346; 73pp; English.
XX
XX The invention relates to a hepatitis B virus (HBV) vaccine composition
CC comprising a pharmaceutical carrier and an isolated peptide less than 25
CC or less than 15 amino acids in length. The invention also relates to a
CC method of inducing a cytotoxic T-cell response to HBV in a mammal and a
CC method of monitoring immunogenic activity of the vaccine in a patient
CC having a known human leukocyte antigen (HLA) type. The composition and
CC methods are useful for preventing and treating HBV infection. This
CC sequence represents an HBV epitope used in the scope of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 8 AA:
SQ
Query Match 40.0%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EYLV 5
DB 5 EYLV 8
```

## RESULT 44

AD205868  
ID AD205868 standard; peptide; 8 AA.

XX AC AD205868;

XX DT 02-JUN-2005 (first entry)

XX DE Hepatitis B virus HLA restricted antigen #1346.

XX KW antiinflammatory; hepatotropic; virucide; vaccine; gene therapy; epitope;  
KW immune response; hepatitis B virus infection.

XX OS Hepatitis B virus.

XX PN US2005063983-A1.

XX PD 24-MAR-2005.

XX PF 04-SEP-2003; 2003US-00654601.

XX PR 05-MAR-1993; 93US-00027146.

XX PR 04-JUN-1993; 93US-00073205.

XX PR 29-NOV-1993; 93US-00159184.

XX PR 04-MAR-1994; 94US-00205713.

XX PR 13-MAR-1996; 96US-0013363P.

XX PR 12-MAR-1997; 97US-00820360.

XX PR 10-NOV-1998; 98US-00189702.

XX PR 27-JAN-1999; 99US-00239043.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Vitello MA, Livingston BD;

XX PI Cells E, Kubo RT, Grey HM, Cheenut RW;

XX DR WPI; 2005-241251/25.

XX PS Claim 47; SEQ ID NO 1346; 497bp; English.

CC The invention relates to a peptide composition, or its analog, of less than 100 amino acid residues comprising a peptide epitope useful for inducing an immune response against hepatitis B virus (HBV). The peptide or peptide epitope comprises an amino acid sequence of about 8-13 or 9-25 amino acid residues that have at least 65% identity with a native amino acid sequence for HBV, and binds to at least one MHC class I or II HLA allele with a dissociation constant of less than about 500 or 1000 nM. The peptide is from the envelope region, polymerase region, protein X region or nucleocapsid core region of HBV. The peptide bears one of the HLA motifs (e.g. HLA A1, HLA A2, HLA A3, HLA A24, HLA B7, HLA B27, HLA B44, HLA B58 or HLA B62 supermotif, or HLA A1, HLA A3, HLA A11 or HLA A24 motif) as listed in the specification. The composition is useful for inducing cellular immune response to HBV or for treating or preventing HBV infection.

XX SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 9; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EYLV 5

DB 5 EYLV 8

## RESULT 45

AD204720  
ID AD204720 standard; peptide; 8 AA.

XX

AC AD204720;

XX DT 02-JUN-2005 (first entry)

XX DE Hepatitis B virus HLA restricted antigen #198.

XX KW antiinflammatory; hepatotropic; virucide; vaccine; gene therapy; epitope;  
KW immune response; hepatitis B virus infection.

XX OS Hepatitis B virus.

XX PN US2005063983-A1.

XX PD 24-MAR-2005.

XX PF 04-SEP-2003; 2003US-00654601.

XX PR 05-MAR-1993; 93US-00027146.

XX PR 04-JUN-1993; 93US-00073205.

XX PR 29-NOV-1993; 93US-00159184.

XX PR 04-MAR-1994; 94US-00205713.

XX PR 13-MAR-1996; 96US-0013363P.

XX PR 12-MAR-1997; 97US-00820360.

XX PR 10-NOV-1998; 98US-00189702.

XX PR 27-JAN-1999; 99US-00239043.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Vitello MA, Livingston BD;

XX PI Cells E, Kubo RT, Grey HM, Cheenut RW;

XX DR WPI; 2005-241251/25.

XX PS Claim 47; SEQ ID NO 198; 497bp; English.

CC The invention relates to a peptide composition, or its analog, of less than 100 amino acid residues comprising a peptide epitope useful for inducing an immune response against hepatitis B virus (HBV). The peptide or peptide epitope comprises an amino acid sequence of about 8-13 or 9-25 amino acid residues that have at least 65% identity with a native amino acid sequence for HBV, and binds to at least one MHC class I or II HLA allele with a dissociation constant of less than about 500 or 1000 nM. The peptide is from the envelope region, polymerase region, protein X region or nucleocapsid core region of HBV. The peptide bears one of the HLA motifs (e.g. HLA A1, HLA A2, HLA A3, HLA A24, HLA B7, HLA B27, HLA B44, HLA B58 or HLA B62 supermotif, or HLA A1, HLA A3, HLA A11 or HLA A24 motif) as listed in the specification. The composition is useful for inducing cellular immune response to HBV or for treating or preventing HBV infection.

XX SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 9; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EYLV 5

DB 5 EYLV 8

## RESULT 46

AEA22285  
ID AEA22285 standard; peptide; 8 AA.

XX AC AEA22285;

XX DT 11-AUG-2005 (first entry)

DE	Soybean activation oxygen inhibiting peptide #3.
XX	
KM	renal hypertension; adrenal hypertension; congestive cardiac failure;
KW	hypotensive; cardiant.
XX	
OS	Glycine max.
XX	
PN	JP2005139158-A.
PD	
XX	02-JUN-2005.
XX	
PF	07-NOV-2003; 2003JP-00413922.
XX	
PR	07-NOV-2003; 2003JP-00413922.
XX	
PA	(SUET/) SUETSUNA Y.
PA	(ORIE-) ORIENTAL BIO KK.
XX	
PI	Suetsuna K, Watanabe K,
XX	
DR	WPI; 2005-390541/40.
XX	
PT	Novel hexapeptide having sequence containing amino acids of L-form, and
PT	capable of inhibiting activity of angiotensin converting enzyme, useful
PT	as angiotensin converting enzyme inhibitor and antihypertensive.
XX	
PS	Disclosure; Page 3; 10pp; Japanese.
XX	
CC	This invention relates to a novel hexapeptide containing amino acids in
CC	the L-form that can be used as an angiotensin converting enzyme (ACE)
CC	inhibitor. Specifically, it refers to a peptide that can be a long-acting
CC	ACE inhibitor as well as an antihypertensive. The present invention
CC	describes using this peptide in pharmaceutical compositions to prevent or
CC	treat hypertension, in particular renal hypertension and adrenal
CC	hypertension, as well as for treating congestive cardiac failure.
CC	Furthermore, the hexapeptide exhibits low toxicity as it does not induce
CC	antibody production and does not generate anaphylactic shock. It also
CC	exhibits hypotensive and cardiant activity in vivo and bradykinin
CC	inactivation inhibitory activity. This peptide sequence is a soybean
CC	activation oxygen inhibition peptide, given in an exemplification of the
CC	invention.
XX	
SO	Sequence 8 AA;
XX	
Query Match	40.0%; Score 4; DB 9; Length 8;
Best Local Similarity	100.0%; Pred.No. 2e+06;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	4 LVPQ 7
XX	
XX	
Db	1 LVPQ 4
XX	
RESULT 47	
AEA90023	
ID	AEA90023 standard; peptide; 8 AA.
XX	
AC	AEA90023;
XX	
DT	25-AUG-2005 (first entry)
XX	
DE	Phage display peptide, SEQ ID NO: 39, with ability to bind Salmonella.
XX	
KM	Phage display; surface display; diagnostic; prognosis;
KW	Salmonella infection; antibacterial; gastrointestinal disease; infection;
XX	gastrointestinal infection; antimicrobial; biosensor.
XX	
OS	unidentified bacteriophage.
XX	
PN	US2005137136-A1.
XX	
PD	23-JUN-2005.
XX	

XX	PF	29-APR-2004; 2004US-00835405.
XX	PR	29-APR-2003; 2003US-0466485P.
XX	PA	(AUBU ) UNIV AUBURN.
PI	P1	Peterenko VA, Sorokulova IB, Chin BA, Barbaree JM, Vodanyoy VJ;
PI	P1	Chen I, Samoylov AM;
DR	WP1:	2005-444162/45.
XX	PT	New biospecific probes, which are synthetic peptides, useful for
PT	PT	identifying bacterial cell surface markers to which the compositions
PT	PT	containing the peptide binds.
XX	PS	Disclosure; SEQ ID NO 39; 25pp; English.
CC	CC	The present invention relates to compositions and methods for binding to
CC	CC	Salmonella bacteria. The compositions comprise peptides which bind to
CC	CC	Salmonella bacteria with high specificity and act as a biospecific probe.
CC	CC	These peptides are cell-binding and cell entry peptides. The invention
CC	CC	includes methods of selecting phages with enhanced binding properties.
CC	CC	These phages display peptides that have stronger and more selective
CC	CC	binding affinity to Salmonella cells. The compositions of the invention
CC	CC	are useful for identifying bacterial cell surface markers to which the
CC	CC	compositions containing the peptide bind. The peptides of the invention
CC	CC	are useful for targeting compounds to Salmonella cells for diagnostic,
CC	CC	prognostic and therapeutic purposes and in the therapy of various
CC	CC	bacterial infections (particularly Salmonella infections which may also
CC	CC	cause food poisoning). The invention is also useful as components of
CC	CC	biosensors for detection and characterization of various cells and cell
CC	CC	populations, in areas of health science and for the production of
CC	CC	biosensitive materials and nanomaterials such as biospecific filters, the
CC	CC	gene- and drug delivery vehicles, hemostatics and molecular switches. The
CC	CC	present sequence is a phase display peptide. This peptide is expressed by
SO	SO	phase selected for ability to bind salmonella.
QY	QY	Sequence 8 AA:
Dy	Dy	Query Match 40.0%; Score 4; DB 9; Length 8;
Dy	Dy	Best Local Similarity 100.0%; Pred. No. 2e+06;
Dy	Dy	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	OY	6 PQQG 9
Dy	Dy	4 PQQG 7
RESULT 48		
ID	ID	AEA90008 standard; peptide; 8 AA.
AC	AC	AEA90008;
XX	XX	25-AUG-2005 (first entry)
DE	DE	Phage display peptide, SEQ ID NO: 24, with ability to bind Salmonella.
KW	KW	Phage display; surface display; diagnostic; prognosis;
KW	KW	gastronella infection; antibacterial; gastrointestinal disease; infection;
OS	OS	gastrointestinal infection; antimicrobial; biosensor.
OS	OS	unidentified bacteriophage.
PN	PN	US2005137136-A1.
PD	PD	23-JUN-2005.
PF	PF	29-APR-2004; 2004US-00835405.
PR	PR	29-APR-2003; 2003US-0466485P.
PA	PA	(AUBU ) UNIV AUBURN.

XX Petrenko VA, Sorokulova IB, Chin BA, Barbaree JM, Vodyanov VJ;  
 PI Chen I, Samoylov AM;  
 XX WPI; 2005-444162/45.  
 XX  
 PT New biospecific probes, which are synthetic peptides, useful for  
 PT identifying bacterial cell surface markers to which the compositions  
 PT containing the peptide binds.  
 PS Disclosure; SEQ ID NO 24; 25pp; English.  
 XX  
 CC The present invention relates to compositions and methods for binding to  
 CC Salmonella bacteria. The compositions comprise peptides which bind to  
 CC Salmonella bacteria with high specificity and act as a biospecific probe.  
 CC These peptides are cell-binding and cell entry peptides. The invention  
 CC includes methods of selecting phages with enhanced binding properties.  
 CC These phages display peptides that have stronger and more selective  
 CC binding affinity to Salmonella cells. The compositions of the invention  
 CC are useful for identifying bacterial cell surface markers to which the  
 CC compositions containing the peptide bind. The peptides of the invention  
 CC are useful for targeting compounds to Salmonella cells for diagnostic,  
 CC prognostic and therapeutic purposes and in the therapy of various  
 CC bacterial infections (particularly Salmonella infections which may also  
 CC cause food poisoning). The invention is also useful as components of  
 CC biosensors for detection and characterization of various cells and cell  
 CC populations, in areas of health science and for the production of  
 CC bioselective materials and nanomaterials such as biospecific filters,  
 CC gene- and drug delivery vehicles, hemostatics and molecular switches. The  
 CC present sequence is a phase display peptide. This peptide is expressed by  
 CC phage selected for ability to bind Salmonella.  
 XX  
 SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQQ 8  
 ||||  
 Db 1 VPQQ 4

# RESULT 49

AEA90030  
 ID AEA90030 standard; peptide; 8 AA.

XX AEA90030;

XX 25-AUG-2005 (first entry)

XX Phage display peptide #1 with ability to bind Salmonella.

XX Phage display; surface display; diagnostic; prognosis;

XX salmonella infection; antibacterial; gastrointestinal disease; infection;

XX gastrointestinal infection; antimicrobial; biosensor.

XX unidentified bacteriophage.

XX US2005137136-A1.

XX 23-JUN-2005.

XX 29-APR-2004; 2004US-00835405.

XX 29-APR-2003; 2003US-0466485P.

XX (AUBU ) UNTV AUBURN.

XX Petrenko VA, Sorokulova IB, Chin BA, Barbaree JM, Vodyanov VJ;

XX PI Chen I, Samoylov AM;

XX WPI; 2005-444162/45.

XX New biospecific probes, which are synthetic peptides, useful for  
 PT identifying bacterial cell surface markers to which the compositions  
 PT containing the peptide binds.  
 PS Disclosure; Page 1; 25pp; English.

XX  
 CC The present invention relates to compositions and methods for binding to  
 CC Salmonella bacteria. The compositions comprise peptides which bind to  
 CC Salmonella bacteria with high specificity and act as a biospecific probe.  
 CC These peptides are cell-binding and cell entry peptides. The invention  
 CC includes methods of selecting phages with enhanced binding properties.  
 CC These phages display peptides that have stronger and more selective  
 CC binding affinity to Salmonella cells. The compositions of the invention  
 CC are useful for identifying bacterial cell surface markers to which the  
 CC compositions containing the peptide bind. The peptides of the invention  
 CC are useful for targeting compounds to Salmonella cells for diagnostic,  
 CC prognostic and therapeutic purposes and in the therapy of various  
 CC bacterial infections (particularly Salmonella infections which may also  
 CC cause food poisoning). The invention is also useful as components of  
 CC biosensors for detection and characterization of various cells and cell  
 CC populations, in areas of health science and for the production of  
 CC bioselective materials and nanomaterials such as biospecific filters,  
 CC gene- and drug delivery vehicles, hemostatics and molecular switches. The  
 CC present sequence is a phase display peptide. This peptide is expressed by  
 CC phage selected for ability to bind Salmonella.  
 XX  
 SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQQ 8  
 ||||  
 Db 1 VPQQ 4

# RESULT 50

AAR39927  
 ID AAR39927 standard; peptide; 9 AA.

XX AAR39927;

XX 25-MAR-2003 (revised)

XX 23-DEC-1993 (first entry)

XX N-terminally guanidinoacyl-modified hirudin deriv. #26.

XX Hirudin analogue; hirulog; leech; anti-coagulant; anti-thrombotic;

XX platelet aggregation inhibition; coagulation; blood clotting.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /label= OTHER

XX Modified-site 2 /note= "(4-guanidino-benzoyl)-Glu"

XX Modified-site 7 /label= OTHER

XX Modified-site 9 /note= "Tyr(MPO3H2), i.e. PO3H2 in meta-position of ring"

XX Misc-difference /note= "D-Glu"

XX EP552999-A1.

XX 28-JUL-1993.

XX 13-JAN-1993; 93BP-00400051.

PR 15-JAN-1992; 92FR-00000340.

XX (ADIR ) ADIR & CIE.

XX Fauchere J, Thurleau C, Verbeuren T, Paladino J;

XX WPI; 1993-23668/30.

DR New stable hirudin deriva. - with increased anticoagulant, antithrombotic  
PT and platelet aggregation inhibiting activities.

XX Example 30; Page 10; 28pp; French.

XX This peptide is a specific example of a highly generic formula for  
CC hirudin analogues. The analogues have antithrombotic, anti-coagulant  
CC and/or platelet aggregation inhibiting activities significantly better  
CC than related known compounds (e.g. at least 30 times greater anti-  
CC coagulant activity than the hirudin 55-65 fragment). Peptides of the  
CC invention also have greater hydrolytic stability and are suitable for  
CC preventing post-thrombotic complications and for inhibiting vascular  
CC wall/platelet interactions implicated in thrombosis and atherosclerosis.  
CC See AAR39903-R39936. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Gaps 0;  
Matches 4; Conservative 0; Indels 0;

QY 1 EEYL 4

DB 5 EEYL 8

Search completed: January 18, 2006, 21:03:09  
Job time : 145 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 20:45:40 ; Search time 16 Seconds

(without alignments)  
1413.184 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EPSRVARDPQRFVIAQNE...AVENPEYLTPOGGAAPQHP 235

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 121454

Minimum DB seq length: 0

Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database: PIR 80:\*

1: PIR1:\*\n2: PIR2:\*\n3: PIR3:\*\n4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	3.0	68	2	LSU ribosomal prot
2	7	3.0	85	2	epidermal growth f
3	7	3.0	105	2	nitrogen fixation
4	7	3.0	120	2	probable regulator
5	7	3.0	138	2	hypothetical prote
6	7	3.0	182	2	NADH2 dehydrogenas
7	7	3.0	197	2	transcription regu
8	7	3.0	212	2	conserved hypothet
9	7	3.0	213	2	regulatory protein
10	7	3.0	220	2	phosphoglucosylase
11	7	3.0	224	2	hypothetical prote
12	7	3.0	229	2	hypothetical prote
13	7	3.0	233	2	hypothetical prote
14	7	3.0	233	2	hypothetical prote
15	6	2.6	24	2	seed protein w8-9
16	6	2.6	26	2	phospholipase A2 (
17	6	2.6	37	2	lipid transfer pro
18	6	2.6	54	2	tetrahydrofolylpol
19	6	2.6	69	2	auxin-induced prot
20	6	2.6	73	2	hypothetical prote
21	6	2.6	73	2	hypothetical prote
22	6	2.6	88	2	cytochrome c6 [val
23	6	2.6	90	2	hypothetical prote
24	6	2.6	92	2	hypothetical prote
25	6	2.6	93	2	hypothetical prote
26	6	2.6	95	2	hypothetical prote
27	6	2.6	96	2	ferredoxin [2Fe-2S
28	6	2.6	97	2	hypothetical prote
29	6	2.6	102	2	hypothetical prote

30	6	2.6	104	2	B42074	hypothetical prote
31	6	2.6	105	1	R1IDS2	somaostatin-22 pr
32	6	2.6	105	2	A45641	acidic ribosomal p
33	6	2.6	106	2	S31435	acidic ribosomal p
34	6	2.6	106	2	S25631	acidic ribosomal p
35	6	2.6	106	2	T48070	hypothetical prote
36	6	2.6	107	1	R50T2R	acidic ribosomal p
37	6	2.6	107	1	R6RM1C	acidic ribosomal p
38	6	2.6	107	2	S59918	acidic ribosomal p
39	6	2.6	107	2	S59913	acidic ribosomal p
40	6	2.6	107	2	S59920	acidic ribosomal p
41	6	2.6	107	2	S59919	acidic ribosomal p
42	6	2.6	107	2	S40106	acidic ribosomal p
43	6	2.6	108	2	H86287	P91.29 protein -
44	6	2.6	109	1	R6TUPJ	acidic ribosomal p
45	6	2.6	109	1	Q0BQZG	Ybab protein - Esc
46	6	2.6	109	2	A40562	conserved hypothet
47	6	2.6	109	2	D90694	hypothetical prote
48	6	2.6	109	2	H85544	hypothetical prote
49	6	2.6	109	2	F81953	hypothetical prote
50	6	2.6	109	2	D81012	hypothetical prote
51	6	2.6	110	2	C71029	hypothetical prote
52	6	2.6	112	1	R6TUTB	acidic ribosomal p
53	6	2.6	113	1	R6TFP2	acidic ribosomal p
54	6	2.6	115	2	T03336	gene e31 protein -
55	6	2.6	115	2	B70536	hypothetical prote
56	6	2.6	115	2	H72745	hypothetical prote
57	6	2.6	119	2	F60767	copla polypeptid
58	6	2.6	119	2	C84403	hypothetical prote
59	6	2.6	120	2	E95329	hypothetical prote
60	6	2.6	120	2	B72519	hypothetical prote
61	6	2.6	122	2	S52840	haloalkanoic acid
62	6	2.6	126	2	H82479	glycine cleavage s
63	6	2.6	127	2	A72488	hypothetical prote
64	6	2.6	127	2	F95976	hypothetical expor
65	6	2.6	130	2	C90503	conserved hypothet
66	6	2.6	130	2	I52612	Landsteiner-Wiener
67	6	2.6	132	2	A11084	hypothetical prote
68	6	2.6	134	2	T44984	methylnalonyl-CoA
69	6	2.6	134	2	H70814	hypothetical prote
70	6	2.6	136	2	T36547	hypothetical prote
71	6	2.6	142	2	UC4997	hypothetical 15.7k
72	6	2.6	144	2	B70111	V-type ATPase, sub
73	6	2.6	145	2	A70576	hypothetical prote
74	6	2.6	147	2	H84047	hypothetical prote
75	6	2.6	149	2	F87569	flagellar basal-bo
76	6	2.6	150	2	A87323	chemotaxis protein
77	6	2.6	150	2	AG1585	hypothetical prote
78	6	2.6	150	2	AH1231	hypothetical prote
79	6	2.6	151	2	AB3643	adhesin aidA-1 [lm
80	6	2.6	153	2	T44492	phosphoenolpyruvat
81	6	2.6	156	2	E84861	hypothetical prote
82	6	2.6	156	2	B72592	hypothetical prote
83	6	2.6	157	2	F71406	hypothetical prote
84	6	2.6	158	2	E87271	hypothetical prote
85	6	2.6	158	2	B71228	hypothetical prote
86	6	2.6	160	2	C72501	hypothetical prote
87	6	2.6	160	2	B82441	conserved hypothet
88	6	2.6	161	2	US0739	H+-transporting tw
89	6	2.6	161	2	F72593	hypothetical prote
90	6	2.6	163	2	B84731	hypothetical prote
91	6	2.6	164	2	F86895	RNA polymerase ECF
92	6	2.6	166	2	S13219	g18 protein - fru1
93	6	2.6	166	2	A45119	basic helix-loop-h
94	6	2.6	167	2	F84559	histone H1 [import
95	6	2.6	167	2	A55438	transcription fact
96	6	2.6	168	2	E87389	RNA polymerase sig
97	6	2.6	169	2	T18321	hypothetical prote
98	6	2.6	170	2	D87707	hypothetical prote
99	6	2.6	171	1	UH0246	phosphotriethic N
100	6	2.6	172	1	AI3475	hypothetical perip
101	6	2.6	173	2	S57617	inorganic diphosph
102	6	2.6	173	2	AG2762	single-strand DNA

103	6	2.6	173	2	T00970	hypothetical prote
104	6	2.6	173	2	A86400	protein F1121.28
105	6	2.6	176	2	AD0261	disulfide bond for
106	6	2.6	180	2	S06616	chorion protein s1
107	6	2.6	181	2	G71171	hypothetical prote
108	6	2.6	181	2	B96025	hypothetical membr
109	6	2.6	182	2	AG0040	single-strand bind
110	6	2.6	183	2	T37084	hypothetical prote
111	6	2.6	183	2	D69108	phycocyanin alpha
112	6	2.6	184	2	D95093	hypothetical prote
113	6	2.6	184	2	A97961	hypothetical prote
114	6	2.6	184	2	T35578	probable secreted
115	6	2.6	186	2	T21961	hypothetical prote
116	6	2.6	188	2	A84383	probable acetyltra
117	6	2.6	188	2	T30389	hypothetical prote
118	6	2.6	190	2	T35381	probable RNA polym
119	6	2.6	191	2	AF0637	probable exported
120	6	2.6	191	2	B83593	conserved hypotet
121	6	2.6	191	2	B64848	yeast protein presu
122	6	2.6	191	2	B90808	hypothetical prote
123	6	2.6	191	2	B95667	hypothetical prote
124	6	2.6	191	2	T47168	hypothetical prote
125	6	2.6	192	2	AD0282	probable exported
126	6	2.6	193	2	AG2033	hypothetical prote
127	6	2.6	194	2	P97543	single-strand bind
128	6	2.6	194	2	C72554	hypothetical prote
129	6	2.6	195	2	A28201	cytochrome b-245 a
130	6	2.6	196	2	S06613	chorion protein s1
131	6	2.6	197	2	S74851	hypothetical prote
132	6	2.6	199	1	A38285	interleukin-11 pre
133	6	2.6	199	2	ACO290	Teer-family transc
134	6	2.6	200	2	S72612	RNA helicase II -
135	6	2.6	200	2	G96564	hypothetical prote
136	6	2.6	203	2	D87567	conserved hypotet
137	6	2.6	203	2	C71812	hypothetical prote
138	6	2.6	203	2	B64706	hypothetical prote
139	6	2.6	203	2	T35866	probable integral
140	6	2.6	203	2	T25916	transcription regu
141	6	2.6	203	2	C83773	conserved hypotet
142	6	2.6	205	2	G90141	chymotrypsin inhib
143	6	2.6	207	2	UX0206	chymotrypsin inhib
144	6	2.6	207	2	US0650	riboflavin synthas
145	6	2.6	208	2	T40995	hypothetical prote
146	6	2.6	208	2	T46927	hypothetical prote
147	6	2.6	208	2	F70734	hypothetical prote
148	6	2.6	208	2	T36390	hypothetical prote
149	6	2.6	208	2	T45272	methyltransferase
150	6	2.6	209	2	T27459	hypothetical prote
151	6	2.6	210	2	B90082	hypothetical prote
152	6	2.6	210	2	G90101	hypothetical prote
153	6	2.6	210	2	B90117	hypothetical prote
154	6	2.6	210	2	B90118	hypothetical prote
155	6	2.6	210	2	B90138	hypothetical prote
156	6	2.6	211	2	T08511	ribn protein - Ent
157	6	2.6	211	2	C96539	hypothetical prote
158	6	2.6	212	2	AD1958	hypothetical prote
159	6	2.6	213	2	SG7811	MG248 homolog H91
160	6	2.6	214	2	AC9684	Rhes family transp
161	6	2.6	215	2	AE1502	hypothetical prote
162	6	2.6	216	2	T14934	hypothetical prote
163	6	2.6	217	2	C81067	ATP phosphoribosyl
164	6	2.6	218	2	SS1751	dihydrodipicolinat
165	6	2.6	218	2	T28689	hypothetical prote
166	6	2.6	219	2	SS5460	beta-tubulin - nem
167	6	2.6	220	2	AI0523	carbonic anhydrase
168	6	2.6	220	2	FA4735	yadF protein - Bsc
169	6	2.6	220	2	B85496	probable carbonate
170	6	2.6	220	2	B90645	probable carbonic
171	6	2.6	220	2	F84565	probable homeodoma
172	6	2.6	220	2	T20880	hypothetical prote
173	6	2.6	221	2	T02666	germin-like protei
174	6	2.6	222	2	H71408	probable germin ty
175	6	2.6	222	2	S71254	germin type 2 - Ar

176	6	2.6	222	2	D69026	conserved hypotet
177	6	2.6	223	2	AG1166	Ribulose-5-Phospha
178	6	2.6	223	2	B84100	cell-division ATP-
179	6	2.6	223	2	T35665	hypothetical prote
180	6	2.6	223	2	AD2793	conserved hypotet
181	6	2.6	224	2	B67949	beta-tubulin ASL1
182	6	2.6	224	2	T02239	germin protein typ
183	6	2.6	224	2	T36146	hypothetical prote
184	6	2.6	224	2	B97466	hypothetical prote
185	6	2.6	225	2	T02660	germin-like protei
186	6	2.6	225	2	T02241	probable germin pr
187	6	2.6	226	2	S77174	nitrate/nitrite re
188	6	2.6	227	2	E25973	pertussis toxin ch
189	6	2.6	227	2	S35240	heat shock protein
190	6	2.6	228	2	B89852	staphylococcal nuc
191	6	2.6	229	2	T05956	germin-like protei
192	6	2.6	231	1	NC5AP	micrococcal nuclea
193	6	2.6	232	1	UH0597	transcription fact
194	6	2.6	232	2	B70653	hypothetical prote
195	6	2.6	232	2	AC2621	conserved hypotet
196	6	2.6	232	2	C97403	hemk protein homol
197	6	2.6	232	2	S75639	cAMP receptor prot
198	6	2.6	234	2	H83138	probable ATP-bindi
199	6	2.6	235	1	CTMSP	corticotropin / 11
200	6	2.6	235	1	CTRTP	corticotropin / 11

## ALIGNMENTS

## RESULT 1

BS9489 LSU ribosomal protein L29P (rpL29P) homolog - Archaeoglobus fulgidus

C.Species: Archaeoglobus fulgidus

C.Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C.Accession: BS9489

R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kiriess, E.F.;

Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A.Author: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Atliach, P.; Kaine, B.P.; Sykes, S.N

Smith, H.O.; Woese, C.R.; Venter, J.C.

A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A.Reference number: A69250; MUID:98049343; PMID:9389475

A.Accession: BS9489

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-68 <KLE>

A.Cross-references: UNIPROT:O28361; UNIPARC:UPI000056B4C; GB:AE000971; GB:AE000782; NID:

C.Superfamily: Escherichia coli ribosomal protein L29

Query Match 3.0%; Score 7; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred.No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 GGAVERN 220  
 |||||  
 Db 38 GGAVERN 44

## RESULT 2

I78540 epidermal growth factor receptor - rhesus macaque (fragment)

C.Species: Macaca mulatta (rhesus macaque)

C.Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Oct-2004

C.Accession: I78540

R.Ma, Y.J.; Costa, M.E.; Ojeda, S.R.

Neuroendocrinology 60, 346-359, 1994

A.Title: Developmental expression of the genes encoding transforming growth factor alpha

A.Reference number: I58134; MUID:95124501; PMID:7545971

A.Accession: I78540

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA



A:Residues: 1-85 <RES>  
A:Cross-references: UNIPROT:P55245; UNIPARC:UPI0000129DF2; GB:S75916; NID:9912829; PIDN:  
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
C:Keywords: ATP; growth factor receptor  
F:1-83/Domain: protein kinase homology (fragment) <KIN>  
Query Match 3.0%; Score 7; DB 2; Length 85;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 MARPDR 11  
Db 79 MARPDR 85

RESULT 3  
A:1985  
nitrogen fixation protein [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AF1985  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21585285; PMID:11759840

A:Accession: AF1985

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q4149; UNIPARC:UPI0000130132; GB:BA000019; PIDN:BAE73390.1;  
A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: nifW

C:Superfamily: nitrogenase stabilizer NifW

Query Match 3.0%; Score 7; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 LVDAERY 49  
Db 11 LVDAERY 17

RESULT 4  
A:1985  
probable regulatory protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T35946

R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1999

A:Reference number: Z21551

A:Accession: T35946

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-120 <SEE>

A:Cross-references: UNIPROT:Q9ZBP4; UNIPARC:UPI00000DAEA2; EMBL:AL035206; PIDN:CAA22768.  
A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC9B5.26c

Query Match 3.0%; Score 7; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 REGPLPA 185  
Db 46 REGPLPA 52

RESULT 5  
A:1985  
hypothetical protein CAC1147 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C:Accession: D97041

R:Rolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D97041

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <KUR>

A:Cross-references: UNIPROT:Q97JX6; UNIPARC:UPI00000CA0DF; GB:AE001437; PIDN:AAK79119.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1147

Query Match 3.0%; Score 7; DB 2; Length 138;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LGLEPSE 93  
Db 37 LGLEPSE 43

RESULT 6  
A:1985

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain C NuoC2 [imported] - Sinorhizobium me

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 31-Dec-2004

C:Accession: H95365

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

.; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.;  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: H95365

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-182 <KUR>

A:Cross-references: UNIPROT:P56896; UNIPARC:UPI00001308AF; GB:AE006469; PIDN:AAK65490.1;  
A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpriel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kise, S.; Komp, C.; Lelaure,  
Hebault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.C.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: nuoC2

A:Genome: plasmid

C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30kD/Ndh/NuoC

C:Keywords: oxidoreductase

Query Match 3.0%; Score 7; DB 2; Length 182;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 FGAVEN 219  
Db 16 FGAVEN 22

RESULT 7

transcription regulator, TetR family beta [imported] - Agrobacterium tumefaciens (strain

```

C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD2829
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Minks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2829
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <KUR>
A:Cross-references: UNIPROT:Q8UDR2; UNIPARC:UPI000016469C; GB:AE008668; PIDN:AAL43050.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: betI
A:Map position: circular chromosome

Query Match      3.0%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      189 AGATLER 195
      |||||
Db      28 AGATLER 34

RESULT 8
AD2595
conserved hypothetical protein Atu0154 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD2595
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Minks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2595
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <KUR>
A:Cross-references: UNIPROT:Q8UIY7; UNIPARC:UPI0000164476; GB:AE008668; PIDN:AAL41178.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0154
A:Map position: circular chromosome
C:Superfamily: hypothetical protein b1832

Query Match      3.0%; Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      118 MGAAGKL 124
      |||||
Db      104 MGAAGKL 110

RESULT 9
B97607
regulatory protein (U73857) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97607
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; William, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

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A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97607
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213 <KUR>
A:Cross-references: UNIPROT:Q8UDR2; UNIPARC:UPI00000DD1D7E; GB:AE007869; PIDN:AAK87811.1;
C:Genetics:
A:Gene: AGR_C_3729
A:Map position: circular chromosome

Query Match      3.0%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      189 AGATLER 195
      |||||
Db      44 AGATLER 50

RESULT 10
AE1802
phosphoglucosyltransferase homolog lin2964 [imported] - Listeria innocua (strain C1p11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1802
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schueller, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <GLA>
A:Cross-references: UNIPROT:Q926S7; UNIPARC:UPI00000CCA28; GB:AL592022; PIDN:CAC98189.1;
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin2964
C:Superfamily: hypothetical protein b2690

Query Match      3.0%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      87 LGLPSE 93
      |||||
Db      162 LGLPSE 168

RESULT 11
E72704
hypothetical protein APE1052 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72704
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72704
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <KAW>
A:Cross-references: UNIPROT:Q9YD60; UNIPARC:UPI000005DDC2; DBJ:AF000060; NID:95104188; I
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1052

```

Query Match 3.0%; Score 7; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 PAPGAG 67  
|||||  
DB 99 PAPGAG 105

## RESULT 12

P97377

hypothetical protein AGR\_C\_252 [imported] - Agrobacterium tumefaciens (strain C58, Cerec  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #ext\_change 09-Jul-2004

C/Accession: F97377  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,  
A.; Liu, F.; Molism, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: F97377  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-229 <KUR>  
A/Cross-references: UNIPROT:Q8UY7; UNIPARC:UPI0000D16F7; GB:AE007869; PIDN:AAK85975.1;  
C/Genetics:  
A/Gene: AGR\_C\_252  
A/Map position: circular chromosome  
C/Superfamily: hypothetical protein b1832

Query Match 3.0%; Score 7; DB 2; Length 229;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 MGAAGL 124  
|||||  
DB 123 MGAAGL 127

## RESULT 13

H96694

hypothetical protein F5A8\_2 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cross)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #ext\_change 05-Oct-2004

C/Accession: H96694  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
Nansen, N.F.; Hughes, B.; Hultzer, L.  
Nature 408, 816-820, 2000  
A/Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurov, J.S.; Malt, R.; Marshall,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Author: Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: H96694  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-233 <STO>  
A/Cross-references: UNIPROT:Q9ZM96; UNIPARC:UPI0000A7A4C; GB:AE051173; NID:94204277; PI  
C/Genetics:  
A/Gene: F5A8\_2  
A/Map position: 1  
C/Superfamily: LOB domain protein

Query Match 3.0%; Score 7; DB 2; Length 233;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LTLGLEP 91  
|||||  
DB 189 LTLGLEP 195

## RESULT 14

I61491

seed protein ws-9 - winged bean (fragment)  
C/Species: Psophocarpus tetragonolobus (winged bean)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #ext\_change 09-Jul-2004  
C/Accession: I61491  
R/Hirano, H.

U/Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dim  
A/Reference number: A61491; MUID:8931606; PMID:2765119  
A/Accession: I61491

A/Status: preliminary  
A/Molecule type: protein

A/Residues: 1-24 <HR>  
A/Cross-references: UNIPROT:Q43708; UNIPARC:UPI00001763AC  
C/Superfamily: plant Kunitz-type proteinase inhibitor  
C/Keywords: seed

Query Match 2.6%; Score 6; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DLVDAB 47  
|||||  
DB 3 DLVDAB 8

## RESULT 15

PQ0725

phospholipase A2 (BC 3.1.1.4) 4.0/15K [imported] - rice (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #ext\_change 09-Jul-2004

C/Accession: PQ0725; PQ0724  
R/Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993

A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
A/Reference number: PQ0696  
A/Accession: PQ0725  
A/Status: preliminary  
A/Molecule type: protein

A/Residues: 1-26 <KOM1>  
A/Cross-references: UNIPROT:Q7MLV0; UNIPARC:UPI000017B114  
A/Accession: PQ0724  
A/Status: preliminary  
A/Molecule type: protein

A/Residues: 1-10 <KOM2>  
A/Cross-references: UNIPARC:UPI000017B115  
C/Keywords: carboxylic ester hydrolase

Query Match 2.6%; Score 6; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 APGAG 67  
|||||  
DB 5 APGAG 10

## RESULT 16

S39036

lipid transfer protein P3 - grape  
C/Species: Vitis sp. (grape)  
C/Date: 25-Dec-1994 #sequence\_revision 19-Apr-1996 #ext\_change 09-Jul-2004

C/Accession: S39036  
R/Coutos-Thévenot, P.; Jouenne, T.; Maes, O.; Guerbette, F.; Grosbois, M.; le Caer, J.P.;  
Bur, J. Biochem. 217, 885-889, 1993  
A/Title: Four 9-kDa proteins excreted by somatic embryos of grapevine are isoforms of 11f  
A/Reference number: S39034; MUID:94039144; PMID:8223644  
A/Accession: S39036  
A/Status: preliminary

A/Molecule type: protein

A:Residues: 1-37 <PGR>  
A:Cross-references: UNIPROT:P80273; UNIPARC:UPI00000330241  
C:Superfamily: phospholipid transfer protein

Query Match 2.6%; Score 6; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GPLPNA 186  
DB 21 GPLPNA 26

## RESULT 17

B66281  
Leutrohydrofolylypolyglutamate synthase (EC 6.3.2.17) - pig (fragments)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
C:Accession: B66281  
R:Garrow, T.A.; Admon, A.; Shane, B.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9151-9155, 1992  
A:Title: Expression cloning of a human cDNA encoding folylpoly(gamma-glutamate) synthetase  
A:Reference number: A66281; MUID:93028422; PMID:1409616  
A:Accession: B66281  
A:Status: preliminary  
A:Molecule type: Protein  
A:Residues: 1-54 <GAR>  
A:Cross-references: UNIPARC:UPI0000088A64  
C:Keywords: ligase

Query Match 2.6%; Score 6; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LTLGLE 90  
DB 28 LTLGLE 33

## RESULT 18

T04350  
auxin-induced protein IAA2 - tomato (fragment)  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04350  
R:Nebentuehr, A.; Lomax, T.L.  
Submitted to the EMBL Data Library, September 1997  
A:Description: Auxin-regulated IeIAA genes of tomato.  
A:Reference number: Z15303  
A:Accession: T04350  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-69 <NEB>  
A:Cross-references: UNIPROT:O64913; UNIPARC:UPI00000ACBAF; EMBL:AF022013; NID:G3043894;  
A:Experimental source: tissue-type etiolated hypocotyls  
C:Genetics:  
A:Gene: IAA2  
C:Superfamily: auxin-induced protein aux28

Query Match 2.6%; Score 6; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 SETDGY 153  
DB 54 SETDGY 59

RESULT 19  
hypothetical protein BH0003 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
\*C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C:Accession: C83650  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and 5  
A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: C83650  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-73 <STO>  
A:Cross-references: UNIPROT:Q9RC40; UNIPARC:UPI00000D4031; GB:AP001507; GB:BA000004; NID:  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH0003

Query Match 2.6%; Score 6; DB 2; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DLVDAE 47  
DB 68 DLVDAE 73

## RESULT 20

B84020  
hypothetical protein BH2962 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: B84020  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and 5  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: B84020  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-73 <STO>  
A:Cross-references: UNIPROT:Q9K8P1; UNIPARC:UPI00000C4076; GB:AP001517; GB:BA000004; NID:  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH2962

Query Match 2.6%; Score 6; DB 2; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLLEBD 38  
DB 20 SLLEBD 25

## RESULT 21

JC5816  
cytochrome c6 [validated] - Chlorella vulgaris (strain CK-22)  
C:Species: Chlorella vulgaris  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
C:Accession: JC5816  
R:Yamada, S.; Nakamura, T.; Tanaka, Y.; Isegai, Y.; Nishio, T.; Oku, T.  
Biosci. Biotechnol. Biochem. 64, 628-632, 2000  
A:Title: Characterization and Amino Acid Sequences of Cytochromes c6 from Two Strains of  
A:Reference number: JC5816  
A:Accession: JC5816  
A:Molecule type: protein  
A:Residues: 1-88 <YAM>  
A:Cross-references: UNIPROT:Q7M1S4; UNIPARC:UPI00000174C7B  
C:Superfamily: cytochrome c6; cytochrome c6 homology  
C:Keywords: acetylated amino end; chromoprotein; electron transfer; heme; iron; metallopro  
F;4-79/Domain: cytochrome c6 homology <CY6>  
F;14,17/Binding site: heme (Yys) (covalent) #status experimental  
F;18,60/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 2.6%; Score 6; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 83 GDLTIG 88  
DB 1 GDLTIG 6

## RESULT 22

T42170  
hypothetical protein L7070 - Escherichia coli plasmid p0157

C/Species: Escherichia coli  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T42170  
R/Burkard, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.  
Nucleic Acids Res. 26, 4196-4204, 1998  
A/Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7  
A/Reference number: Z22068; MWID:98391744; PMID:9722640  
A/Accession: T42170  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-90 <BUR>  
A/Cross-references: UNIPROT:Q9ZGSS; UNIPARC:UPI000003811; EMBL:AF074613; PIDD:AACT0138.  
A/Experimental source: strain EDJ933; serotype O157:H7  
C/Genetics:  
A/Genome: plasmid p0157  
A/Note: L7070

Query Match 2.6%; Score 6; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 RSSSTR 79  
DB 59 RSSSTR 64

## RESULT 23

D84330  
hypothetical protein Vng1786h [imported] - Halobacterium sp. NRC-1

C/Species: Halobacterium sp. NRC-1  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: D84330  
R/Ng, W.V.; Kennedy, S.P.; Mahafes, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laeky, S.; Leibauner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabit Jung, K.H.; Alam, M.; Prells, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A/Title: Genome sequence of Halobacterium species NRC-1.  
A/Reference number: A84160; MWID:20504483; PMID:11016950  
A/Accession: D84330  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-92 <STO>  
A/Cross-references: UNIPROT:Q9HP62; UNIPARC:UPI0000063985; GB:AE004437; MID:910581240; F  
C/Genetics:  
A/Genome: Vng1786h

Query Match 2.6%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 DPORPV 13  
DB 41 DPORPV 46

## RESULT 24

S42743  
hypothetical protein - Erwinia chrysanthemi (fragment)

C/Species: Erwinia chrysanthemi  
C/Date: 07-Oct-1994 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
C/Accession: S42743  
R/Moulard, M.; Condemine, G.; Robert-Baudouy, J.

Mol. Microbiol. 8, 685-695, 1993  
A/Title: Characterization of the nuc gene coding for a nuclease of the phytopathogenic  
A/Reference number: S34943; MWID:93323747; PMID:8332061  
A/Accession: S42743  
A/Status: preliminary; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-93 <MOU>  
A/Cross-references: UNIPROT:P37995; UNIPARC:UPI000013B096; EMBL:X73255; MID:9403001; PIDD  
C/Superfamily: methyltransferase, b1r0722 type

Query Match 2.6%; Score 6; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 223 LTPQGG 228  
DB 12 LTPQGG 17

## RESULT 25

D69121  
hypothetical protein MTH1905 - Methanobacterium thermoautotrophicum (strain Delta H)

C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: D69121  
R/Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi  
A/Reference number: A69000; MWID:98037514; PMID:9371463  
A/Accession: D69121  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-95 <MTH>  
A/Cross-references: UNIPROT:Q27927; UNIPARC:UPI0000062C1A; GB:AE000941; GB:AE000666; MID:  
A/Experimental source: strain Delta H  
C/Genetics:  
A/Genome: MTH1905  
A/Start codon: GTG  
C/Superfamily: hypothetical protein MTH1905

Query Match 2.6%; Score 6; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLLEDD 38  
DB 62 SLLEDD 67

## RESULT 26

F70379  
ferredoxin [2Fe-2S] fdx1 [similarity] - Aquifex aeolicus

C/Species: Aquifex aeolicus  
C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C/Accession: F70379  
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Ove  
V.  
Nature 392, 353-358, 1998  
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A/Reference number: A70300; MWID:98196666; PMID:9537320  
A/Accession: F70379  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-96 <AQF>  
A/Cross-references: UNIPROT:Q67065; UNIPARC:UPI0000056444; GB:AE000713; MID:92983424; PII  
A/Experimental source: strain VFS  
C/Genetics:  
A/Genome: fdx1

C/Superfamily: ferredoxin (2Fe-2S)  
C/Keywords: 2Fe-2S; iron-sulfur protein; metalloprotein  
F/21-79/Domain: ferredoxin [2Fe-2S] homology <FER>

F,34,39,42,78/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 2.6%; Score 6; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 EPSEEE 95  
|||||  
DB 55 EPSEEE 60

RESULT 27  
S11755

hypothetical protein - Plasmodium vivax (fragment)

C.Species: Plasmodium vivax  
C.Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C.Accession: S11755

R.Campbell, J.R.; Franke, E.D.

submitted to the EMBL Data Library, April 1989

A.Description: A repetitive element found in Plasmodium vivax DNA.

A.Reference number: S11755

A.Accession: S11755

A.Molecule type: DNA

A.Residues: 1-97 <C&M>

A.Cross-references: UNIPROT:Q26168; UNIPARC:UPI000007CFDD; EMBL:X15129; NID:g10086; PID:

Query Match 2.6%; Score 6; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 APSEGA 107  
|||||  
DB 29 APSEGA 34

RESULT 28  
P97780

hypothetical protein RC0646 [imported] - Rickettsia conorii (strain Malish 7)

C.Species: Rickettsia conorii

C.Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004

C.Accession: P97780

R.Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001

A.Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A.Reference number: A97700; MUID:21442074; PMID:11557893

A.Accession: P97780

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-97 <KUR>

A.Cross-references: UNIPROT:Q92HX4; UNIPARC:UPI00000CBE59; GB:AE006914; PIDN:AAL03184.1;

A.Gene: RC0646

Query Match 2.6%; Score 6; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 TIGLEP 91  
|||||  
DB 37 TIGLEP 42

RESULT 29  
E72482

hypothetical protein APE2501 - Aeropyrum pernix (strain KL)

C.Species: Aeropyrum pernix

C.Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C.Accession: E72482

R.Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A.Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A.Reference number: A72450; MUID:99310339; PMID:10382966

A.Accession: E72482

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-102 <K&M>

A.Cross-references: UNIPROT:Q9Y8Y3; UNIPARC:UPI000005E389; DDBJ:AP000064; NID:g5105945; I

A.Experimental source: strain KL

C.Genetics:

A.Gene: APE2501

C.Superfamily: Aeropyrum pernix hypothetical protein APE2501

Query Match 2.6%; Score 6; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TRSGGG 83  
|||||  
DB 12 TRSGGG 17

RESULT 30  
E42074

hypothetical protein 2 (SMP1 gene region) - human

C.Species: Homo sapiens (man)

C.Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004

C.Accession: E42074

R.Schuchman, E.H.; Levran, O.; Pereira, L.V.; Deanick, R.J.

Genomics 12, 197-205, 1992

A.Title: Structural organization and complete nucleotide sequence of the gene encoding h

A.Reference number: A42074; MUID:92155708; PMID:1740330

A.Accession: E42074

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: DNA

A.Residues: 1-104 <SCH>

A.Cross-references: UNIPROT:Q15495; UNIPARC:UPI00006D406; GB:M81780; NID:g972768; PIDN:f

C.Superfamily: human hypothetical protein 2 (SMP1 gene region)

Query Match 2.6%; Score 6; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 APGAGG 67  
|||||  
DB 6 APGAGG 11

RESULT 31  
R11DS2

somatostatin-22 precursor - channel catfish

N.Alternate names: somatostatin II; SST-22

N.Contains: somatostatin-22

C.Species: Ictalurus punctatus (channel catfish)

C.Date: 02-Apr-1982 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C.Accession: S00293; A92451; A92271; I50799; A01436

R.Magazin, M.; Minch, C.D.; Funke, C.L.; Deechene, R.; Tavlanini, M.A.; Dixon, J.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 5152-5156, 1982

A.Title: Sequence of a cDNA encoding pancreatic preprosomatostatin-22.

A.Reference number: S00293; MUID:83039328; PMID:6127673

A.Accession: S00293

A.Molecule type: mRNA

A.Residues: 1-105 <MAG>

A.Cross-references: UNIPROT:P01172; UNIPARC:UPI0000135AD6; GB:J00945; NID:g213341; PIDN:f

R.Andrews, P.C.; Pubols, M.H.; Hermanson, M.A.; Shearer, B.T.; Dixon, J.E.

J. Biol. Chem. 259, 13267-13272, 1984

A.Title: Structure of the 22-residue somatostatin from catfish. An O-glycosylated peptide

A.Reference number: A92451; MUID:85030447; PMID:6149220

A.Accession: A92451

A.Molecule type: protein

A.Residues: 84-105 <AND>

A.Cross-references: UNIPARC:UPI00001733D5

A.Note: this is the major form of somatostatin-22

R.Oyama, H.; Bradshaw, R.A.; Bates, O.J.; Permutt, A.

J. Biol. Chem. 255, 2251-2254, 1980

A.Title: Amino acid sequence of catfish pancreatic somatostatin I.

A/Reference number: A92271; MUID:80137439; PMID:7358665  
A/Accession: A92271  
A/Molecule type: protein  
A/Residues: 1-4, 'R', '6-18, 'S', '20-22 <OYA>  
A/Cross-references: UNIPARC:UPI00001733D6  
A/Experimental source: pancreatic islet D-cell  
A/Note: the authors' designation of this form as somatostatin I may conflict with other  
R.Dixon, J.E.; Andrews, P.C.  
Adv. Exp. Med. Biol. 188, 19-29, 1985  
A/Title: Somatostatins of the channel catfish.  
A/Reference number: 150798; MUID:85303576; PMID:2863931  
A/Accession: 150799  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-105 <DIX>  
A/Cross-references: UNIPARC:UPI0000135AD6; GB:M25904; NID:G213343; PIDN:AAA49341.1; PID:  
C/Superfamily: somatostatin  
C/Keyword: glycoprotein; neuropeptide; pancreatic islet  
F/1-25/Domain: signal sequence #status predicted <SIG>  
F/26-33/Domain: propeptide #status predicted <PRO>  
F/34-105/Product: somatostatin-22 #status experimental <MAT>  
F/88/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F/94-105/Disulfide bonds: #status experimental

Query Match 2.6%; Score 6; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EEDPRS 99  
DB 71 EEDPRS 76

RESULT 32  
A45641  
acidic ribosomal protein P2 - Trypanosoma cruzi (fragment)  
C/Species: Trypanosoma cruzi  
C/Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
R/Matizger, D.A.; Reinos, R.F.; Hunter, C.A.; Donelson, J.E.  
Mol. Biochem. Parasitol. 49, 325-328, 1991  
A/Title: Patients infected with Leishmania donovani chagasi can have antibodies that rec  
A/Reference number: A45641; MUID:92131069; PMID:1733150  
A/Accession: A45641  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-105 <NRP>  
A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B3; GB:M72710; GB:M72712; NID:G16  
A/Note: sequence extracted from NCBI backbone (NCBI:79052, NCBI:P:79054)  
C/Superfamily: rat acidic ribosomal protein P1

Query Match 2.6%; Score 6; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41  
DB 95 EDDDMG 100

RESULT 33  
S31435  
acidic ribosomal protein P2 isoform P-JL5 - Trypanosoma cruzi (fragment)  
C/Species: Trypanosoma cruzi  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S31435  
R/Schijman, A.G.  
Submitted to the EMBL Data Library, September 1992  
A/Reference number: S31435  
A/Accession: S31435  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-106 <SCH>

A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B3; EMBL:X69508; NID:G10643; PIDN:  
C/Superfamily: rat acidic ribosomal protein P1

Query Match 2.6%; Score 6; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41  
DB 96 EDDDMG 101

RESULT 34  
S25631  
acidic ribosomal protein P2 isoform P2a-RA - Trypanosoma cruzi  
C/Species: Trypanosoma cruzi  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
R/Vazquez, M.; Levin, M.J.  
Submitted to the EMBL Data Library, September 1992  
A/Reference number: S25631  
A/Accession: S25631  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-106 <VAZ>  
A/Cross-references: UNIPROT:Q26944; UNIPARC:UPI000007C407; EMBL:X68310; NID:G10631; PIDN:  
C/Superfamily: rat acidic ribosomal protein P1

Query Match 2.6%; Score 6; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41  
DB 97 EDDDMG 102

RESULT 35  
T48070  
hypothetical protein F26K9.240 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C/Accession: T48070  
R/Bioecker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Queirer, F.; Salanoubat  
Submitted to the Protein Sequence Database, March 2000  
A/Reference number: Z24465  
A/Accession: T48070  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-106 <BLO>  
A/Cross-references: UNIPROT:Q9LZ14; UNIPARC:UPI000000C46C; EMBL:AL162651  
A/Experimental source: cultivar Columbia; BAC clone P26K9  
C/Genetics:  
A/Map position: 3  
A/Intons: 81/1  
A/Note: F26K9.240

Query Match 2.6%; Score 6; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AGATLE 194  
DB 89 AGATLE 94

RESULT 36  
R5UT28  
acidic ribosomal protein P2-A - Trypanosoma cruzi  
N/Alternate names: acidic ribosomal protein P-JL5; ribosomal protein TL12el; Tcp2-beta  
C/Species: Trypanosoma cruzi  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C/Accession: S12585; A60447; S59917

R;Schijman, A.G.; Dusetci, N.J.; Vazquez, M.P.; Lafon, S.; Levy-Yeyati, P.; Levin, M.J.  
Nucleic Acids Res. 18, 3399, 1990  
A>Title: Nucleotide cDNA and complete deduced amino acid sequence of a Trypanosoma cruzi  
A/Reference number: S12585; MUID:90287723; PMID:2192363  
A/Accession: S12585  
A/Molecule type: mRNA  
A/Residues: 1-107 <SCH>  
A/Cross-references: UNIPROT:P23632; UNIPARC:UPI0000134263; EMBL:X52323; NID:G10635; PIDN  
R;Levin, M.J.; Meiri, E.; Benarous, R.; Levitus, G.; Schijman, A.; Levy-Yeyati, P.; Chis  
Am. J. Trop. Med. Hyg. 41, 530-538, 1989  
A>Title: Identification of major Trypanosoma cruzi antigenic determinants in chronic cha  
A/Reference number: A60447; MUID:90053984; PMID:2479275  
A/Accession: A60447  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 73-83, 'G', 85-107 <LEV>  
A/Cross-references: UNIPARC:UPI0000173AB8  
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.  
Biochim. Biophys. Acta 1264, 15-18, 1995  
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru  
A/Reference number: S59912; MUID:96038812; PMID:7578249  
A/Accession: S59912  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-107 <SC2>  
A/Cross-references: UNIPARC:UPI0000134263; EMBL:X52323; NID:G10635; PIDN:CAA36557.1; PID  
C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41  
DB 97 EDDDMG 102

RESULT 37  
REMIC  
acidic ribosomal protein P1, cytosolic - Chlamydomonas reinhardtii  
C/Species: Chlamydomonas reinhardtii  
C/Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
C/Accession: S24990  
R;Dumont, F.  
submitted to the EMBL Data Library, May 1992  
A/Reference number: S24989  
A/Accession: S24990  
A/Molecule type: mRNA  
A/Residues: 1-107 <DUM>  
A/Cross-references: UNIPROT:P29763; UNIPARC:UPI0000134241; EMBL:X66411; NID:G18210; PIDN  
C/Superfamily: rat acidic ribosomal protein P1  
C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 EPSSEER 95  
DB 94 EPSSEER 99

RESULT 38  
S59918  
acidic ribosomal protein P2.beta (H1.5) - Trypanosoma cruzi  
N/Alternate names: acidic ribosomal protein P.1J5 variant D  
C/Species: Trypanosoma cruzi  
C/Date: 24-Aug-1996 #sequence\_revision 08-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: S59918; S40100; S31434  
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.  
Biochim. Biophys. Acta 1264, 15-18, 1995  
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru

A/Reference number: S59912; MUID:96038812; PMID:7578249  
A/Accession: S59918  
A/Molecule type: mRNA  
A/Residues: 1-107 <SCH>  
A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016COB8; EMBL:X69510; NID:G10639; PIDN  
R;Vazquez, M.; Schijman, A.; Levin, M.  
submitted to the EMBL Data Library, September 1993  
A/Reference number: S40100  
A/Accession: S40100  
A/Molecule type: DNA  
A/Residues: 1-107 <VAZ>  
A/Cross-references: UNIPARC:UPI000016COB8; EMBL:X75030; NID:G436137; PIDN:CAA52938.1; PII  
C/Superfamily: rat acidic ribosomal protein P1  
C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41  
DB 97 EDDDMG 102

RESULT 39  
S59913  
acidic ribosomal protein P2.beta (H1.3) - Trypanosoma cruzi  
C/Species: Trypanosoma cruzi  
C/Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S59913  
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.  
Biochim. Biophys. Acta 1264, 15-18, 1995  
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru  
A/Reference number: S59912; MUID:96038812; PMID:7578249  
A/Accession: S59913  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-107 <SCH>  
A/Cross-references: UNIPROT:Q26959; UNIPARC:UPI00001772PE  
C/Superfamily: rat acidic ribosomal protein P1  
C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41  
DB 97 EDDDMG 102

RESULT 40  
S59920  
acidic ribosomal protein P2.beta (H6.4) - Trypanosoma cruzi  
C/Species: Trypanosoma cruzi  
C/Date: 24-Aug-1996 #sequence\_revision 08-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: S59920; S40103  
R;Schijman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghio, S.; Lorenzi, H.; Levin, M.J.  
Biochim. Biophys. Acta 1264, 15-18, 1995  
A>Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru  
A/Reference number: S59912; MUID:96038812; PMID:7578249  
A/Accession: S59920  
A/Molecule type: mRNA  
A/Residues: 1-107 <SCH>  
A/Cross-references: UNIPROT:Q26957; UNIPARC:UPI00000817CC; EMBL:X75031; NID:G436141; PIDN  
R;Vazquez, M.; Schijman, A.; Levin, M.  
submitted to the EMBL Data Library, September 1993  
A/Reference number: S40100  
A/Accession: S40103  
A/Molecule type: DNA  
A/Residues: 1-107 <VAZ>  
A/Cross-references: UNIPARC:UPI00000817CC; EMBL:X75031; NID:G436141; PIDN:CAA52941.1; PII  
C/Superfamily: rat acidic ribosomal protein P1



C;Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41

Db 97 EDDDMG 102

RESULT 41

559919

acidic ribosomal protein p2.beta (X) - Trypanosoma cruzi

N/Alternate names: acidic ribosomal protein P.1J5 variant C

C/Species: Trypanosoma cruzi

C/Date: 24-Aug-1996 #sequence\_revision 08-Nov-1996 #text\_change 09-Jul-2004

C/Accession: S59919; S31433

R/Schjman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghilo, S.; Lorenzi, H.; Levin, M.J.

Blochm. Biophys. Acta 1264, 15-18, 1995

A/Title: Cloning and sequence analysis of the Tcp2-beta cDNA variants of Trypanosoma cru

A/Reference number: S59912; PMID:96038812; PMID:7578249

A/Accession: S59919

A/Molecule type: mRNA

A/Residues: 1-107 <SCH>

A/Cross-references: UNIPROT:P23632; UNIPARC:UPI000016C0B7; EMBL:X65509; NID:G10637; PIDN

C/Superfamily: rat acidic ribosomal protein P1

C/Keywords: phosphoprotein; protein biosynthesis; ribosome

Query Match 2.6%; Score 6; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMG 41

Db 97 EDDDMG 102

RESULT 42

540106

acidic ribosomal protein p2.beta (H1.8) - Trypanosoma cruzi

N/Alternate names: gene Tcp2beta protein

C/Species: Trypanosoma cruzi

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C/Accession: S40106; S59912; S40107

R/Vazquez, M.; Schjman, A.; Levin, M.

submitted to the EMBL Data Library, September 1993

A/Reference number: S40106

A/Accession: S40106

A/Molecule type: DNA

A/Residues: 1-107 <VAZ>

A/Cross-references: UNIPROT:Q27291; UNIPARC:UPI0000079E46; EMBL:X75033; NID:G436148; PIDN

R/Schjman, A.G.; Vazquez, M.P.; Ben Dov, C.; Ghilo, S.; Lorenzi, H.; Levin, M.J.

us-09-930-125-2\_copy\_975\_1209.oligo.rpr

Page 11

RESULT 43

H86287

P9L1.29 protein - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: H86287

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Maltz, R.; Marzall,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; PMID:121016719; PMID:11130712

A/Accession: H86287

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <STO>

A/Cross-references: UNIPROT:Q9X135; UNIPARC:UPI000000BEB8; GB:AE005172; NID:G5103833; PIDN

C/Genetics:

A/Map position: 1

Query Match 2.6%; Score 6; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 PEYVNG 168

Db 32 PEYVNG 37

RESULT 44

R6UTP1

acidic ribosomal protein P1 - Trypanosoma cruzi

C/Species: Trypanosoma cruzi

C/Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

C/Accession: S22644; S19924

R/Vazquez, M.P.; Schjman, A.G.; Levin, M.J.

Nucleic Acids Res. 20, 2599, 1992

A/Title: Nucleotide sequence of a cDNA encoding a Trypanosoma cruzi acidic ribosomal P1

A/Reference number: S22644; PMID:92285148; PMID:1598221

A/Accession: S22644

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-109 <VAZ>

us-09-930-125-2\_copy\_975\_1209.oligo.rpr

Page 11

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us-09-930-125-2\_copy\_975\_1209.oligo.rpr

A:Residues: 1-109 <MAH>  
A:Cross-references: UNIPROT:P17577; UNIPARC:UPI000005A1P2; GB:M38777; NID:G145295; PIDN:  
R:Flower, A.M.; McHenry, C.S.  
Nucleic Acids Res. 14, 8091-8101, 1986  
A:Title: The adjacent dna2 and dna3 genes of *Escherichia coli* are contained within one c  
A:Reference number: A25549; MUID:87040775; PMID:3534795  
A:Accession: C25549  
A:Molecule type: DNA  
A:Residues: 1-75 <ELO>  
A:Cross-references: UNIPARC:UPI000016F6F4; GB:X04487; NID:G43319; PIDN:CA28176.1; PID:G  
A:Experimental source: strain K-12, substrain JM109  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of *Escherichia coli* K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: F64777  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-109 <BLAT>  
A:Cross-references: UNIPARC:UPI000005A1P2; GB:AE000153; GB:U00096; NID:G1786671; PIDN:AF  
A:Experimental source: strain K-12, substrain MG1655  
A:Genetics:  
A:Gene: ybaB  
A:Map position: 11 min  
C:Superfamily: uncharacterized conserved protein

Query Match 2.6%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38  
|||||  
60 SLEDD 65

Db 60 SLEDD 65

RESULT 46  
AH0562  
conserved hypothetical protein STY0529 [imported] - *Salmonella enterica* subsp. *enterica*  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A:Note: this species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 31-Dec-2004  
C:Accession: AH0562  
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AH0562  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109 <PAR>  
A:Cross-references: UNIPARC:UPI000005A1P2; GB:AL513382; PIDN:CAD04970.1; PID:G16501756;  
C:Genetics:  
A:Gene: STY0529  
C:Superfamily: uncharacterized conserved protein

Query Match 2.6%; Score 6; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38  
|||||  
60 SLEDD 65

Db 60 SLEDD 65

RESULT 47  
D90694  
hypothetical protein EG0524 [imported] - *Escherichia coli* (strain O157:H7, substrain R1  
C:Species: *Escherichia coli*  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 31-Dec-2004

C:Accession: D90694  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
Gasaara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genom  
A:Reference number: A9629; MUID:21156231; PMID:11258796  
A:Accession: D90694  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109 <HAY>  
A:Cross-references: UNIPROT:P17577; UNIPARC:UPI000005A1P2; GB:BA000007; PIDN:BA33947.1;  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: EG0524  
C:Superfamily: uncharacterized conserved protein

Query Match 2.6%; Score 6; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38  
|||||  
60 SLEDD 65

Db 60 SLEDD 65

RESULT 48  
H85544  
hypothetical protein ybaB [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933  
C:Species: *Escherichia coli*  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Dec-2004  
C:Accession: H85544  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Diallantha, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: H85544  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109 <STO>  
A:Cross-references: UNIPROT:P17577; UNIPARC:UPI000005A1P2; GB:AE005174; NID:G12513341; P1  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ybaB  
C:Superfamily: uncharacterized conserved protein

Query Match 2.6%; Score 6; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLEDD 38  
|||||  
60 SLEDD 65

Db 60 SLEDD 65

RESULT 49  
F81953  
hypothetical protein MMA0376 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup  
C:Species: *Neisseria meningitidis*  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: F81953  
R:Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell  
A.; Holroyd, S.; Jagsall, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: F81953  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109 <PAR>  
A:Cross-references: UNIPROT:Q9JMG9; UNIPARC:UPI00000C4970; GB:AL162753; GB:AL157959; NID:  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:

A:Gene: NMA0376

Query Match 2.6%; Score 6; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YRSILE 36  
|||||  
DB 83 YRSILE 88

RESULT 50

D81012  
hypothetical protein NMB2059 [imported] - Neisseria meningitidis (strain MCS8 serogroup  
C/Species: Neisseria meningitidis  
C/Date: 31-Mar-2000 #sequence\_revulsion 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: D81012  
R/Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
rt, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.  
Science 287, 1809-1815, 2000  
A/Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
A/Reference number: A81000; WUID:20175755; PMID:10710307  
A/Accession: D81012  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-109 <TET>  
A/Cross-references: UNIPROT:Q9JXG7; UNIPARC:UPI00000C4858; GB:AE002555; GB:AE002098; NID  
A/Experimental source: serogroup B, strain MCS8  
C/Genetics:  
A:Gene: NMB2059

Query Match 2.6%; Score 6; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YRSILE 36  
|||||  
DB 83 YRSILE 88

Search completed: January 18, 2006, 20:49:39  
Job time : 29 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 21:06:00 : Search time 111 Seconds  
(without alignments)  
37.642 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 10  
Sequence: 1 ERYLVPQGF 10

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 0  
Total number of hits satisfying chosen parameters: 232507

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database:

Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubppa/us07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/us08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/us09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/us10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/us10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/us11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	US-09-930-125-3	Sequence 3, Appl1
2	10	100.0	10	US-10-313-644-3	Sequence 3, Appl1
3	9	90.0	9	US-10-245-871-607	Sequence 607, App
4	9	90.0	9	US-10-149-138-1138	Sequence 1138, Ap
5	9	90.0	9	US-10-149-138-3666	Sequence 3666, Ap
6	9	90.0	9	US-10-253-286-607	Sequence 607, App
7	9	90.0	9	US-10-149-138-1138	Sequence 1138, Ap
8	9	90.0	9	US-10-149-138-3666	Sequence 3666, Ap
9	9	90.0	10	US-10-149-138-1139	Sequence 1139, Ap
10	9	90.0	10	US-10-149-138-3667	Sequence 3667, Ap
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14	8	80.0	8	US-10-149-138-1449	Sequence 1449, Ap
15	8	80.0	8	US-10-149-138-2377	Sequence 2377, Ap
16	8	80.0	8	US-10-149-138-15	Sequence 15, Appl1
17	8	80.0	8	US-10-149-138-1449	Sequence 1449, Ap
18	8	80.0	8	US-10-149-138-2377	Sequence 2377, Ap
19	8	80.0	8	US-10-149-138-2377	Sequence 2377, Ap
20	8	80.0	8	US-10-149-138-2377	Sequence 2377, Ap
21	8	80.0	9	US-10-149-138-45	Sequence 45, Appl1
22	8	80.0	9	US-10-149-138-1450	Sequence 1450, Ap
23	8	80.0	9	US-10-149-138-2378	Sequence 2378, Ap
24	8	80.0	9	US-10-149-138-3171	Sequence 3171, Ap
25	8	80.0	9	US-10-149-138-45	Sequence 45, Appl1
26	8	80.0	9	US-10-149-138-1450	Sequence 1450, Ap
27	8	80.0	9	US-10-149-138-2378	Sequence 2378, Ap

28	8	80.0	9	US-10-149-138-3171	Sequence 3171, Ap
29	8	80.0	10	US-10-333-430-64	Sequence 64, Appl1
30	7	70.0	8	US-10-149-138-25	Sequence 25, Appl1
31	7	70.0	8	US-10-149-138-1249	Sequence 1249, Ap
32	7	70.0	8	US-10-149-138-2188	Sequence 2188, Ap
33	7	70.0	8	US-10-149-138-2859	Sequence 2859, Ap
34	7	70.0	8	US-10-149-138-25	Sequence 25, Appl1
35	7	70.0	8	US-10-149-138-1249	Sequence 1249, Ap
36	7	70.0	8	US-10-149-138-2188	Sequence 2188, Ap
37	7	70.0	8	US-10-149-138-2859	Sequence 2859, Ap
38	6	60.0	9	US-10-149-138-4152	Sequence 4152, Ap
39	6	60.0	9	US-10-149-138-4152	Sequence 4152, Ap
40	5	50.0	9	US-10-149-138-506	Sequence 506, App
41	5	50.0	9	US-10-149-138-2183	Sequence 2183, Ap
42	5	50.0	9	US-10-149-138-506	Sequence 506, App
43	5	50.0	9	US-10-149-138-2183	Sequence 2183, Ap
44	5	50.0	10	US-10-149-138-220	Sequence 2046, App
45	5	50.0	10	US-10-149-138-2046	Sequence 2046, App
46	5	50.0	10	US-10-149-138-220	Sequence 2046, App
47	5	50.0	10	US-10-149-138-2046	Sequence 2046, App
48	4	40.0	5	US-09-912-733-4	Sequence 4, Appl1
49	4	40.0	6	US-10-209-323-4	Sequence 4, Appl1
50	4	40.0	6	US-10-256-277-4	Sequence 4, Appl1
51	4	40.0	8	US-10-149-138-505	Sequence 505, App
52	4	40.0	8	US-10-149-138-1246	Sequence 1246, App
53	4	40.0	8	US-10-149-138-505	Sequence 505, App
54	4	40.0	8	US-10-149-138-1246	Sequence 1246, App
55	4	40.0	8	US-10-654-601-198	Sequence 198, App
56	4	40.0	8	US-10-654-601-1346	Sequence 1346, App
57	4	40.0	8	US-10-835-405-24	Sequence 24, Appl1
58	4	40.0	8	US-10-835-405-39	Sequence 39, Appl1
59	4	40.0	9	US-08-812-393A-62	Sequence 62, Appl1
60	4	40.0	9	US-09-354-533-23	Sequence 23, Appl1
61	4	40.0	9	US-09-899-235-28	Sequence 28, Appl1
62	4	40.0	9	US-09-793-451-21	Sequence 21, Appl1
63	4	40.0	9	US-09-793-451-126	Sequence 126, App
64	4	40.0	9	US-09-793-451-126	Sequence 126, App
65	4	40.0	9	US-09-793-451-230	Sequence 230, App
66	4	40.0	9	US-09-793-451-323	Sequence 323, App
67	4	40.0	9	US-09-793-451-464	Sequence 464, App
68	4	40.0	9	US-09-793-451-552	Sequence 552, App
69	4	40.0	9	US-09-793-451-660	Sequence 660, App
70	4	40.0	9	US-09-774-681-62	Sequence 62, Appl1
71	4	40.0	9	US-09-984-365-40	Sequence 40, Appl1
72	4	40.0	9	US-09-984-365-41	Sequence 41, Appl1
73	4	40.0	9	US-10-238-607-41	Sequence 41, Appl1
74	4	40.0	9	US-10-238-607-41	Sequence 41, Appl1
75	4	40.0	9	US-10-405-231-40	Sequence 40, Appl1
76	4	40.0	9	US-10-405-231-41	Sequence 41, Appl1
77	4	40.0	9	US-10-283-722-21	Sequence 21, Appl1
78	4	40.0	9	US-10-283-722-126	Sequence 126, App
79	4	40.0	9	US-10-283-722-221	Sequence 221, App
80	4	40.0	9	US-10-283-722-230	Sequence 230, App
81	4	40.0	9	US-10-283-722-323	Sequence 323, App
82	4	40.0	9	US-10-283-722-464	Sequence 464, App
83	4	40.0	9	US-10-283-722-552	Sequence 552, App
84	4	40.0	9	US-10-283-722-660	Sequence 660, App
85	4	40.0	9	US-10-283-903-21	Sequence 21, Appl1
86	4	40.0	9	US-10-283-903-126	Sequence 126, App
87	4	40.0	9	US-10-283-903-221	Sequence 221, App
88	4	40.0	9	US-10-283-903-323	Sequence 323, App
89	4	40.0	9	US-10-283-903-323	Sequence 323, App
90	4	40.0	9	US-10-283-903-464	Sequence 464, App
91	4	40.0	9	US-10-283-903-552	Sequence 552, App
92	4	40.0	9	US-10-283-903-660	Sequence 660, App
93	4	40.0	9	US-10-149-138-219	Sequence 219, App
94	4	40.0	9	US-10-149-138-1098	Sequence 1098, App
95	4	40.0	9	US-10-647-005-23	Sequence 23, Appl1
96	4	40.0	9	US-10-643-888-37	Sequence 37, Appl1
97	4	40.0	9	US-10-643-888-38	Sequence 38, Appl1
98	4	40.0	9	US-10-643-888-59	Sequence 59, Appl1
99	4	40.0	9	US-10-643-888-60	Sequence 60, Appl1
100	4	40.0	9	US-10-643-888-61	Sequence 61, Appl1

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102	4	40.0	9	4	US-10-643-888-63	Sequence 63, App1
103	4	40.0	9	4	US-10-643-888-64	Sequence 64, App1
104	4	40.0	9	4	US-10-643-888-69	Sequence 69, App1
105	4	40.0	9	4	US-10-643-888-70	Sequence 70, App1
106	4	40.0	9	4	US-10-643-888-71	Sequence 71, App1
107	4	40.0	9	4	US-10-643-888-72	Sequence 72, App1
108	4	40.0	9	4	US-10-149-138-219	Sequence 219, App1
109	4	40.0	9	4	US-10-149-138-1098	Sequence 1098, App1
110	4	40.0	9	4	US-10-697-055-40	Sequence 40, App1
111	4	40.0	9	4	US-10-697-055-41	Sequence 41, App1
112	4	40.0	9	5	US-10-474-960A-376	Sequence 376, App
113	4	40.0	9	5	US-10-736-640-40	Sequence 40, App1
114	4	40.0	9	5	US-10-736-640-41	Sequence 41, App1
115	4	40.0	9	5	US-10-654-601-698	Sequence 698, App
116	4	40.0	9	5	US-10-654-601-1313	Sequence 1313, App
117	4	40.0	9	5	US-10-654-601-2018	Sequence 2018, App
118	4	40.0	9	6	US-11-121-347-23	Sequence 23, App1
119	4	40.0	10	3	US-09-793-451-178	Sequence 178, App
120	4	40.0	10	3	US-09-793-451-200	Sequence 200, App
121	4	40.0	10	3	US-09-793-451-475	Sequence 475, App
122	4	40.0	10	3	US-09-793-451-481	Sequence 481, App
123	4	40.0	10	3	US-09-793-451-487	Sequence 487, App
124	4	40.0	10	3	US-09-793-451-603	Sequence 603, App
125	4	40.0	10	3	US-09-793-451-611	Sequence 611, App
126	4	40.0	10	4	US-10-283-723-178	Sequence 178, App
127	4	40.0	10	4	US-10-283-723-200	Sequence 200, App
128	4	40.0	10	4	US-10-283-723-475	Sequence 475, App
129	4	40.0	10	4	US-10-283-723-481	Sequence 481, App
130	4	40.0	10	4	US-10-283-723-487	Sequence 487, App
131	4	40.0	10	4	US-10-283-723-603	Sequence 603, App
132	4	40.0	10	4	US-10-283-723-611	Sequence 611, App
133	4	40.0	10	4	US-10-371-525-200	Sequence 200, App
134	4	40.0	10	4	US-10-371-525-200	Sequence 200, App
135	4	40.0	10	4	US-10-371-645-200	Sequence 200, App
136	4	40.0	10	4	US-10-283-903-178	Sequence 178, App
137	4	40.0	10	4	US-10-283-903-200	Sequence 200, App
138	4	40.0	10	4	US-10-283-903-475	Sequence 475, App
139	4	40.0	10	4	US-10-283-903-481	Sequence 481, App
140	4	40.0	10	4	US-10-283-903-487	Sequence 487, App
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142	4	40.0	10	4	US-10-283-903-611	Sequence 611, App
143	4	40.0	10	4	US-10-371-260-200	Sequence 200, App
144	4	40.0	10	4	US-10-149-138-642	Sequence 642, App
145	4	40.0	10	4	US-10-634-262-22	Sequence 22, App1
146	4	40.0	10	4	US-10-149-138-642	Sequence 642, App
147	4	40.0	10	5	US-10-654-601-699	Sequence 699, App
148	4	40.0	10	5	US-10-654-601-2019	Sequence 2019, App
149	4	40.0	10	5	US-10-654-601-2462	Sequence 2462, App
150	4	40.0	10	5	US-10-654-601-2549	Sequence 2549, App
151	3	30.0	3	3	US-09-820-306-66	Sequence 66, App1
152	3	30.0	4	2	US-08-424-550B-538	Sequence 538, App
153	3	30.0	4	3	US-09-778-885-11	Sequence 11, App1
154	3	30.0	4	3	US-09-234-395-25	Sequence 25, App1
155	3	30.0	4	3	US-09-234-395-26	Sequence 26, App1
156	3	30.0	4	3	US-09-305-928-25	Sequence 25, App1
157	3	30.0	4	3	US-09-305-928-26	Sequence 26, App1
158	3	30.0	4	3	US-09-819-136-6	Sequence 6, App1
159	3	30.0	4	3	US-09-264-516A-51	Sequence 51, App1
160	3	30.0	4	4	US-09-264-516A-52	Sequence 52, App1
161	3	30.0	4	4	US-10-021-963-7	Sequence 7, App1
162	3	30.0	4	4	US-10-006-869-86	Sequence 86, App1
163	3	30.0	4	4	US-10-006-869-87	Sequence 87, App1
164	3	30.0	4	4	US-10-006-869-142	Sequence 142, App
165	3	30.0	4	4	US-10-006-869-144	Sequence 144, App
166	3	30.0	4	4	US-10-006-869-362	Sequence 362, App
167	3	30.0	4	4	US-10-006-869-364	Sequence 364, App
168	3	30.0	4	4	US-10-141-357-51	Sequence 51, App1
169	3	30.0	4	4	US-10-141-357-52	Sequence 52, App1
170	3	30.0	4	4	US-10-395-032-86	Sequence 86, App1
171	3	30.0	4	4	US-10-395-032-87	Sequence 87, App1
172	3	30.0	4	4	US-10-95-032-142	Sequence 142, App
173	3	30.0	4	4	US-10-95-032-144	Sequence 144, App

174330.044US-10-395-032-362Sequence 362, App

175330.044US-10-395-032-364Sequence 364, App

176330.044US-10-301-849A-14Sequence 14, App1

177330.044US-10-661-819-5Sequence 5, App1

178330.044US-10-654-578-1952Sequence 1952, App

179330.044US-10-654-578-1953Sequence 1953, App

180330.044US-10-759-379-25Sequence 25, App1

181330.044US-10-759-379-26Sequence 26, App1

182330.044US-10-759-507-25Sequence 25, App1

183330.044US-10-759-507-26Sequence 26, App1

184330.044US-10-864-087-15Sequence 15, App1

185330.044US-10-864-087-16Sequence 16, App1

186330.044US-10-946-789-10Sequence 10, App1

187330.044US-10-946-441-17Sequence 17, App1

188330.044US-10-946-441-42Sequence 42, App1

189330.044US-10-946-441-43Sequence 43, App1

190330.044US-10-946-441-173Sequence 17, App1

191330.044US-10-946-441-174Sequence 17, App1

192330.044US-10-946-441-175Sequence 17, App1

193330.044US-10-946-441-176Sequence 17, App1

194330.044US-10-946-441-177Sequence 17, App1

195330.044US-10-946-441-178Sequence 17, App1

196330.044US-10-946-441-179Sequence 17, App1

197330.044US-10-946-441-180Sequence 17, App1

198330.044US-10-946-441-181Sequence 17, App1

199330.044US-10-946-441-182Sequence 17, App1

200330.044US-10-946-441-183Sequence 17, App1

RESULT 1

US-09-930-125-3

Sequence 3, Application US/09930125

Publication No. US200201933229A1

GENERAL INFORMATION:

APPLICANT: Hand-Zimmerman, Susan

APPLICANT: Cheever, Martin A.

APPLICANT: Foy, Teresa M.

APPLICANT: Lodes, Michael J.

APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Vedick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

FILE REFERENCE: 210121.544

CURRENT APPLICATION NUMBER: US/09/930.125

CURRENT FILING DATE: 2001-08-14

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 10

TYPE: PRT

ORGANISM: Homo sapiens

US-09-930-125-3

Query Match100.0%; Score 10; DB 3; Length 10;

Best Local Similarity100.0%; Pred. No. 0.00028;

Matches10; Conservative0; Mismatches0; Indels0; Gaps0;

Oy1BEYLVPOOGF10

Db1BEYLVPOOGF10

RESULT 2

US-10-313-644-3

Sequence 3, Application US/10313644

Publication No. US20030157119A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Cheever, Martin A.

APPLICANT: Hand-Zimmerman, Susan  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL  
FILE REFERENCE: 210121.483C3  
CURRENT APPLICATION NUMBER: US/10/313,644  
CURRENT FILING DATE: 2002-12-04  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-313-644-3

Query Match 100.0%; Score 10; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00028;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1 EYLVPOQGF 10

RESULT 3  
US-10-245-871-607  
Sequence 607, Application US/10245871  
Publication No. US20030235594A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: I1-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: RH-2013  
CURRENT APPLICATION NUMBER: US/10/245,871  
CURRENT FILING DATE: 2003-01-09  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 607  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-245-871-607

Query Match 90.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10  
Db 1 EYLVPOQGF 9

RESULT 4  
US-10-149-138-1138  
Sequence 1138, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Pike, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esben  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1138  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-1138

Query Match 90.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10  
Db 1 EYLVPOQGF 9

RESULT 5  
US-10-149-138-3666  
Sequence 3666, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Pike, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esben  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3666  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3666

Query Match 90.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10  
Db 1 EYLVPOQGF 9

RESULT 6  
US-10-253-286-607  
Sequence 607, Application US/10253286  
Publication No. US20040058881A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: I1-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: RH-2015  
CURRENT APPLICATION NUMBER: US/10/253,286  
CURRENT FILING DATE: 2003-01-13

/ PRIOR APPLICATION NUMBER: 10/197,000  
/ PRIOR FILING DATE: 2002-07-17  
/ PRIOR APPLICATION NUMBER: 09/396,813  
/ PRIOR FILING DATE: 1999-09-14  
/ NUMBER OF SEQ ID NOS: 905  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 607  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-253-286-607

Query Match 90.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10  
DB 1 EYLVPQGGF 9

RESULT 7  
US-10-149-138-1138  
/ Sequence 1138, Application US/10149138  
/ Publication No. US20040121946A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Fikes, John  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Celis, Esteban  
/ APPLICANT: Keogh, Elissa  
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1138  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-1138

Query Match 90.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10  
DB 1 EYLVPQGGF 9

RESULT 8  
US-10-149-138-3666  
/ Sequence 3666, Application US/10149138  
/ Publication No. US20040121946A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Fikes, John  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Celis, Esteban  
/ APPLICANT: Keogh, Elissa

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 3666  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3666

Query Match 90.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10  
DB 1 EYLVPQGGF 9

RESULT 9  
US-10-149-138-1139  
/ Sequence 1139, Application US/10149138  
/ Publication No. US20040018971A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Fikes, John  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Celis, Esteban  
/ APPLICANT: Keogh, Elissa  
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1139  
/ LENGTH: 10  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-1139

Query Match 90.0%; Score 9; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPQGGF 10  
DB 1 EYLVPQGGF 9

RESULT 10  
US-10-149-138-3667  
/ Sequence 3667, Application US/10149138  
/ Publication No. US20040018971A1  
/ GENERAL INFORMATION:



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/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3667
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3667

Query Match          90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 11
US-10-149-138-1139
/ Sequence 1139, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1139
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1139

Query Match          90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9
```

```

RESULT 12
US-10-149-138-3667
/ Sequence 3667, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3667
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3667

Query Match          90.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 1 EYLVPOQGF 9

RESULT 13
US-10-149-138-15
/ Sequence 15, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-15
```

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
|||  
1 YLVPOQGF 8

## RESULT 14

US-10-149-138-1449

; Sequence 1449, Application US/10149138  
; Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1449

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-1449

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
|||  
1 YLVPOQGF 8

## RESULT 15

US-10-149-138-2377

; Sequence 2377, Application US/10149138  
; Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2377

; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2377

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
|||  
1 YLVPOQGF 8

## RESULT 16

US-10-149-138-3170

; Sequence 3170, Application US/10149138  
; Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3170

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3170

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
|||  
1 YLVPOQGF 8

## RESULT 17

US-10-149-138-15

; Sequence 15, Application US/10149138  
; Publication No. US20040121946A9

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0140001

CURRENT FILING DATE: 2002-06-10

/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 15  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
/ US-10-149-138-15

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 18  
US-10-149-138-1449  
/ Sequence 1449, Application US/10149138  
/ Publication No. US20040121946A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Fikes, John  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Cellis, Esteban  
/ APPLICANT: Keogh, Elissa

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1449  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
/ US-10-149-138-1449

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 19  
US-10-149-138-2377  
/ Sequence 2377, Application US/10149138  
/ Publication No. US20040121946A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Fikes, John  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Chesnut, Robert

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1449  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
/ US-10-149-138-1449

/ APPLICANT: Cellis, Esteban  
/ APPLICANT: Keogh, Elissa  
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2377  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
/ US-10-149-138-2377

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 20  
US-10-149-138-3170  
/ Sequence 3170, Application US/10149138  
/ Publication No. US20040121946A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Fikes, John  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Cellis, Esteban  
/ APPLICANT: Keogh, Elissa  
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to  
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0140001  
/ CURRENT APPLICATION NUMBER: US/10/149,138  
/ CURRENT FILING DATE: 2002-06-10  
/ PRIOR APPLICATION NUMBER: PCT/US00/33591  
/ PRIOR FILING DATE: 2000-12-11  
/ PRIOR APPLICATION NUMBER: US 09/458,299  
/ PRIOR FILING DATE: 1999-12-11  
/ NUMBER OF SEQ ID NOS: 4641  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 3170  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Artificially Synthesized Peptide  
/ US-10-149-138-3170

Query Match 80.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 21  
US-10-149-138-45  
/ Sequence 45, Application US/10149138

```
Publication No. US20040018971A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-45
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 YLVPQGGF 10
        |||||
DB      1 YLVPQGGF 8
```

```
RESULT 22
US-10-149-138-1450
Sequence 1450, Application US/10149138
Publication No. US20040018971A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1450
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1450
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 YLVPQGGF 10
```

```
DB      1 YLVPQGGF 8
        |||||
```

```
RESULT 23
US-10-149-138-2378
Sequence 2378, Application US/10149138
Publication No. US20040018971A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2378
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2378
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 YLVPQGGF 10
        |||||
DB      1 YLVPQGGF 8
```

```
RESULT 24
US-10-149-138-3171
Sequence 3171, Application US/10149138
Publication No. US20040018971A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3171
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptide
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 YLVPQGGF 10
```

US-10-149-138-3171

Query Match 80.0%; Score 8; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 25

US-10-149-138-45  
Sequence 45, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Basteen  
APPLICANT: Keogh, Elisha  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 45  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-45

Query Match 80.0%; Score 8; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 26

US-10-149-138-1450  
Sequence 1450, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Basteen  
APPLICANT: Keogh, Elisha  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1450  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-1450

Query Match 80.0%; Score 8; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 27

US-10-149-138-2378  
Sequence 2378, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Basteen  
APPLICANT: Keogh, Elisha  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2378  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2378

Query Match 80.0%; Score 8; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
Db 1 YLVPOQGF 8

RESULT 28

US-10-149-138-3171  
Sequence 3171, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Basteen  
APPLICANT: Keogh, Elisha  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001

```
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3171
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3171
```

```
Query Match      80.0%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 YLVPOQGF 10
Db      1 YLVPOQGF 8
```

```
RESULT 29
US-10-333-430-64
/ Sequence 64, Application US/10/333430
/ Publication No. US20040072240A1
/ GENERAL INFORMATION:
/ APPLICANT: INSERM
/ APPLICANT: INSTITUT GUSTAVE ROUSSY
/ APPLICANT: KOSMOTOPOULOS, Kostas
/ APPLICANT: TOUNDOR, Sophie
/ APPLICANT: SCARDINO, Antonio
/ APPLICANT: GROSS, David, Alexandre
/ TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
/ FILE REFERENCE: 33339/259034
/ CURRENT APPLICATION NUMBER: US/10/333,430
/ CURRENT FILING DATE: 2003-10-02
/ PRIOR APPLICATION NUMBER: FR 0009591
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 64
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
US-10-333-430-64
```

```
Query Match      80.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 YLVPOQGF 10
Db      1 YLVPOQGF 8
```

```
RESULT 30
US-10-149-138-25
/ Sequence 25, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
```

```
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 25
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-25
```

```
Query Match      70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 LVPQGGF 10
Db      1 LVPQGGF 7
```

```
RESULT 31
US-10-149-138-1249
/ Sequence 1249, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1249
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-1249
```

```
Query Match      70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 LVPQGGF 10
Db      1 LVPQGGF 7
```

```
RESULT 32
US-10-149-138-2188
/ Sequence 2188, Application US/10149138
/ Publication No. US20040018971A1
```

GENERAL INFORMATION:  
APPLICANT: Pike, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Eteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2188  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2188

Query Match 70.0%; Score 7; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10  
DB 1 LVPOQGF 7

RESULT 33  
US-10-149-138-2859  
Sequence 2859, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Pike, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Eteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2859  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2859

Query Match 70.0%; Score 7; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LVPOQGF 10  
DB 1 LVPOQGF 7

DB 1 LVPOQGF 7  
RESULT 34  
US-10-149-138-25  
Sequence 25, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Pike, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Eteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 25  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-25

Query Match 70.0%; Score 7; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10  
DB 1 LVPOQGF 7

RESULT 35  
US-10-149-138-1249  
Sequence 1249, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Pike, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Eteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1249  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-1249

Query Match 70.0%; Score 7; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10  
|||  
DB 1 LVPOQGF 7

RESULT 36  
US-10-149-138-2188  
; Sequence 2188, Application US/10149138  
; Publication No. US20040121946A9

GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elisea  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2188  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2188

Query Match 70.0%; Score 7; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10  
|||  
DB 1 LVPOQGF 7

RESULT 37  
US-10-149-138-2859  
; Sequence 2859, Application US/10149138  
; Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elisea  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2859  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2859

Query Match 70.0%; Score 7; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVPOQGF 10  
|||  
DB 1 LVPOQGF 7

RESULT 38  
US-10-149-138-4152  
; Sequence 4152, Application US/10149138  
; Publication No. US20040018971A1

GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elisea  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4152  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-4152

Query Match 60.0%; Score 6; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEYLYP 6  
|||  
DB 4 BEYLYP 9

RESULT 39  
US-10-149-138-4152  
; Sequence 4152, Application US/10149138  
; Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elisea  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138



```

/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4152
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4152

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 EBYLV 6
DB 4 EBYLV 9

RESULT 40
US-10-149-138-506
/ Sequence 506, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HRR2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 506
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-506

Query Match
Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 EBYLV 5
DB 5 EBYLV 9

RESULT 41
US-10-149-138-2183
/ Sequence 2183, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
```

```

/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HRR2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2183
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2183

Query Match
Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 EBYLV 5
DB 5 EBYLV 9

RESULT 42
US-10-149-138-506
/ Sequence 506, Application US/10149138
/ Publication No. US20040121946A3
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HRR2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 506
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-506

Query Match
Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 EBYLV 5
DB 5 EBYLV 9

RESULT 43
US-10-149-138-2183
```

```
/ Sequence 2183, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2183
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2183
```

```
Query Match 50.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EBYLV 5
Db 5 EBYLV 9
```

```
RESULT 44
US-10-149-138-220
/ Sequence 220, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 220
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-220
```

```
Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EBYLV 5
Db 6 EBYLV 10
```

```
RESULT 45
US-10-149-138-2046
/ Sequence 2046, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2046
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2046
```

```
Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 EBYLV 5
Db 6 EBYLV 10
```

```
RESULT 46
US-10-149-138-220
/ Sequence 220, Application US/10149138
/ Publication No. US20040121946A9
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Keogh, Elissa
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/new Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 220
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
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OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-220

Query Match 50.0%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLV 5  
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Db 6 EBYLV 10

RESULT 47  
US-10-149-138-2046

Sequence 2046, Application US/10149138  
Publication No. US20040121946A9  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Betteban  
APPLICANT: Keogh, Elisea  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 2046  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2046

Query Match 50.0%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLV 5  
| | | | |  
Db 6 EBYLV 10

RESULT 48  
US-09-912-733-4

Sequence 4, Application US/09912733  
Publication No. US20030092131A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Michael  
APPLICANT: Power, Scott D.  
TITLE OF INVENTION: POLYPEPTIDES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF  
TITLE OF INVENTION: POLYPEPTIDES IN FILAMENTOUS FUNGI  
FILE REFERENCE: A-62926-1  
CURRENT APPLICATION NUMBER: US/09/912,733  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 08/785,668  
PRIOR FILING DATE: 1997-01-17  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Synthetic.  
US-09-912-733-4

Query Match 40.0%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
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Db 2 EBYL 5

RESULT 49  
US-10-209-323-4

Sequence 4, Application US/10209323  
Publication No. US20030119070A1  
GENERAL INFORMATION:  
APPLICANT: Schaeffer, Andrew T.  
APPLICANT: Tseng-Law, Janet  
APPLICANT: Thornton, Jeffrey R.  
APPLICANT: Van Bpps, Dennis E.  
TITLE OF INVENTION: Reagents For Cell Selection and Methods  
TITLE OF INVENTION: Of Use  
FILE REFERENCE: P-N74360  
CURRENT APPLICATION NUMBER: US/10/209,323  
CURRENT FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US/09/659,469A  
PRIOR FILING DATE: 2000-09-11  
PRIOR APPLICATION NUMBER: US 09/578,784  
PRIOR FILING DATE: 2000-05-23  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-209-323-4

Query Match 40.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QOGP 10  
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Db 1 QOGP 4

RESULT 50  
US-10-256-277-4

Sequence 4, Application US/10256277  
Publication No. US20030219445A1  
GENERAL INFORMATION:  
APPLICANT: Schaeffer, Andrew T.  
APPLICANT: Tseng-Law, Janet  
APPLICANT: Thornton, Jeffrey R.  
TITLE OF INVENTION: Reagents For Cell Selection and Methods  
TITLE OF INVENTION: Of Use  
FILE REFERENCE: P-NT 3773  
CURRENT APPLICATION NUMBER: US/10/256,277  
CURRENT FILING DATE: 2002-09-25  
PRIOR APPLICATION NUMBER: US/09/578,784  
PRIOR FILING DATE: 2000-05-23  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-256-277-4

Query Match 40.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QGGF 10  
|||  
Db 1 QGGF 4

Search completed: January 18, 2006, 21:17:06  
Job time : 113 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 21:00:09 : Search time 44 Seconds  
(without alignments)  
18.790 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 10

Sequence: 1 EBYLVPOQGF 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 0

Total number of hits satisfying chosen parameters: 130918

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database: Issued Patents AA:\*

- 1: /cgnt2\_6/prodata/1/1aa/5 COMB.pep:\*
- 2: /cgnt2\_6/prodata/1/1aa/6 COMB.pep:\*
- 3: /cgnt2\_6/prodata/1/1aa/H COMB.pep:\*
- 4: /cgnt2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*
- 5: /cgnt2\_6/prodata/1/1aa/RB COMB.pep:\*
- 6: /cgnt2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	50.0	9	4	PCT-US93-01669-56	Sequence 56, Appl
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4	40.0	5	2	US-09-912-733-4	Sequence 4, Appl
5	40.0	6	2	US-09-581-944A-25	Sequence 25, Appl
6	40.0	7	2	US-09-147-933-19	Sequence 19, Appl
7	40.0	7	2	US-09-581-944A-20	Sequence 20, Appl
8	40.0	7	6	5422249-15	Patent No. 5422249
9	40.0	8	1	US-08-037-574A-7	Sequence 7, Appl
10	40.0	8	1	US-08-037-574A-9	Sequence 9, Appl
11	40.0	8	1	US-08-037-574A-13	Sequence 13, Appl
12	40.0	8	1	US-08-037-574A-17	Sequence 17, Appl
13	40.0	8	1	US-08-037-574A-79	Sequence 79, Appl
14	40.0	8	1	US-08-037-574A-81	Sequence 81, Appl
15	40.0	8	1	US-08-037-574A-83	Sequence 83, Appl
16	40.0	8	1	US-08-037-574A-100	Sequence 100, Appl
17	40.0	8	1	US-08-037-574A-106	Sequence 106, Appl
18	40.0	8	1	US-08-037-574A-114	Sequence 114, Appl
19	40.0	8	1	US-08-037-574A-118	Sequence 118, Appl
20	40.0	8	1	US-08-037-574A-151	Sequence 151, Appl
21	40.0	8	1	US-08-037-574A-157	Sequence 157, Appl
22	40.0	8	1	US-08-037-574A-163	Sequence 163, Appl
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27	40.0	8	1	US-08-218-329-79	Sequence 79, Appl

28	40.0	8	1	US-08-218-329-81	Sequence 81, Appl
29	40.0	8	1	US-08-218-329-83	Sequence 83, Appl
30	40.0	8	1	US-08-218-329-99	Sequence 99, Appl
31	40.0	8	1	US-08-218-329-105	Sequence 105, Appl
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33	40.0	8	1	US-08-218-329-117	Sequence 117, Appl
34	40.0	8	1	US-08-218-329-150	Sequence 150, Appl
35	40.0	8	1	US-08-218-329-156	Sequence 156, Appl
36	40.0	8	1	US-08-218-329-162	Sequence 162, Appl
37	40.0	8	1	US-08-482-228-117	Sequence 117, Appl
38	40.0	8	2	US-08-482-528-117	Sequence 117, Appl
39	40.0	8	2	US-09-239-043D-198	Sequence 1346, Ap
40	40.0	8	2	US-09-239-043D-1346	Patent No. 5196404
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42	40.0	9	1	US-08-467-083-23	Sequence 23, Appl
43	40.0	9	1	US-08-414-417B-23	Sequence 23, Appl
44	40.0	9	1	US-08-486-348A-23	Sequence 23, Appl
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57	40.0	9	2	US-09-692-325-70	Sequence 70, Appl
58	40.0	9	2	US-09-692-325-71	Sequence 71, Appl
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61	40.0	9	2	US-09-239-043D-698	Sequence 698, Ap
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63	40.0	9	2	US-09-239-043D-2018	Sequence 2018, Ap
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66	40.0	9	2	US-10-238-607-40	Sequence 40, Appl
67	40.0	9	2	US-10-238-607-41	Sequence 41, Appl
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70	40.0	9	2	US-10-697-055-40	Sequence 40, Appl
71	40.0	9	2	US-10-697-055-41	Sequence 41, Appl
72	40.0	9	2	US-10-697-055-47	Sequence 47, Appl
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77	40.0	9	2	US-10-643-888-61	Sequence 61, Appl
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80	40.0	9	2	US-10-643-888-64	Sequence 64, Appl
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83	40.0	9	2	US-10-643-888-71	Sequence 71, Appl
84	40.0	9	2	US-10-643-888-72	Sequence 72, Appl
85	40.0	10	1	US-08-325-253-11	Sequence 11, Appl
86	40.0	10	1	US-08-368-542C-22	Sequence 22, Appl
87	40.0	10	2	US-09-475-316A-40	Sequence 40, Appl
88	40.0	10	2	US-09-111-784A-200	Sequence 200, Appl
89	40.0	10	2	US-09-704-640-40	Sequence 40, Appl
90	40.0	10	2	US-09-554-467A-22	Sequence 22, Appl
91	40.0	10	2	US-09-239-043D-699	Sequence 699, Appl
92	40.0	10	2	US-09-239-043D-2019	Sequence 2019, Ap
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94	40.0	10	2	US-09-239-043D-2549	Sequence 2549, Ap
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96	40.0	10	2	US-09-660-302B-32	Sequence 32, Appl
97	30.0	4	1	US-07-906-349A-16	Sequence 16, Appl
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99	30.0	4	1	US-08-102-757-23	Sequence 23, Appl
100	30.0	4	1	US-08-167-035-16	Sequence 16, Appl

101	3	30.0	4	1	US-08-255-272-21	Sequence 21, Appl	174	3	30.0	5	2	US-09-020-880-45	Sequence 45, Appl
102	3	30.0	4	1	US-08-208-887A-16	Sequence 16, Appl	175	3	30.0	5	2	US-09-273-565-63	Sequence 63, Appl
103	3	30.0	4	1	US-08-625-322-5	Sequence 5, Appl	176	3	30.0	5	2	US-08-505-250-31	Sequence 31, Appl
104	3	30.0	4	1	US-07-963-538B-8	Sequence 8, Appl	177	3	30.0	5	2	US-08-605-430-51	Sequence 51, Appl
105	3	30.0	4	1	US-08-539-005-15	Sequence 15, Appl	178	3	30.0	5	2	US-08-505-250-31	Sequence 31, Appl
106	3	30.0	4	2	US-09-039-308A-17	Sequence 17, Appl	179	3	30.0	5	2	US-09-565-538-63	Sequence 63, Appl
107	3	30.0	4	2	US-09-320-095-11	Sequence 11, Appl	180	3	30.0	5	2	US-09-368-449B-41	Sequence 41, Appl
108	3	30.0	4	2	US-09-523-487-11	Sequence 11, Appl	181	3	30.0	5	2	US-09-020-065A-3	Sequence 3, Appl
109	3	30.0	4	2	US-09-187-859-86	Sequence 86, Appl	182	3	30.0	5	2	US-09-187-859-88	Sequence 88, Appl
110	3	30.0	4	2	US-09-187-859-87	Sequence 87, Appl	183	3	30.0	5	2	US-09-187-859-89	Sequence 89, Appl
111	3	30.0	4	2	US-09-187-859-142	Sequence 142, App	184	3	30.0	5	2	US-09-187-859-143	Sequence 91, Appl
112	3	30.0	4	2	US-09-187-859-144	Sequence 144, App	185	3	30.0	5	2	US-09-187-859-145	Sequence 145, App
113	3	30.0	4	2	US-09-187-859-362	Sequence 362, App	186	3	30.0	5	2	US-09-187-859-147	Sequence 147, App
114	3	30.0	4	2	US-09-187-859-364	Sequence 364, App	187	3	30.0	5	2	US-09-187-859-363	Sequence 363, App
115	3	30.0	4	2	US-09-388-183-7	Sequence 7, Appl	188	3	30.0	5	2	US-09-187-859-365	Sequence 365, App
116	3	30.0	4	2	US-09-280-598-16	Sequence 16, Appl	189	3	30.0	5	2	US-09-187-859-367	Sequence 367, App
117	3	30.0	4	2	US-09-578-303-15	Sequence 15, Appl	190	3	30.0	5	2	US-09-187-859-736	Sequence 736, App
118	3	30.0	4	2	US-09-240-179-32	Sequence 32, Appl	191	3	30.0	5	2	US-09-187-859-751	Sequence 751, App
119	3	30.0	4	2	US-09-305-927-51	Sequence 51, Appl	192	3	30.0	5	2	US-09-187-859-766	Sequence 766, App
120	3	30.0	4	2	US-09-305-927-52	Sequence 52, Appl	193	3	30.0	5	2	US-09-187-859-796	Sequence 796, App
121	3	30.0	4	2	US-08-469-260A-538	Sequence 538, App	194	3	30.0	5	2	US-09-187-859-811	Sequence 811, App
122	3	30.0	4	2	US-09-584-001C-17	Sequence 17, Appl	195	3	30.0	5	2	US-09-187-859-812	Sequence 812, App
123	3	30.0	4	2	US-09-584-001C-28	Sequence 28, Appl	196	3	30.0	5	2	US-09-187-859-814	Sequence 814, App
124	3	30.0	4	2	US-09-584-001C-43	Sequence 43, Appl	197	3	30.0	5	2	US-09-187-859-1050	Sequence 1050, App
125	3	30.0	4	2	US-08-488-446-538	Sequence 538, App	198	3	30.0	5	2	US-09-187-859-1094	Sequence 1094, App
126	3	30.0	4	2	US-09-839-542B-86	Sequence 86, Appl	199	3	30.0	5	2	US-09-187-859-1138	Sequence 1138, App
127	3	30.0	4	2	US-09-839-542B-87	Sequence 87, Appl	200	3	30.0	5	2		
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142	3	30.0	4	2	US-09-580-893D-17	Sequence 17, Appl							
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144	3	30.0	4	2	US-09-580-893D-42	Sequence 42, Appl							
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148	3	30.0	4	2	US-09-580-110E-43	Sequence 43, Appl							
149	3	30.0	4	2	US-09-176-664-53	Sequence 53, Appl							
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154	3	30.0	4	2	US-09-580-156D-43	Sequence 43, Appl							
155	3	30.0	4	2	US-10-006-869-87	Sequence 86, Appl							
156	3	30.0	4	2	US-10-006-869-88	Sequence 87, Appl							
157	3	30.0	4	2	US-10-006-869-142	Sequence 142, App							
158	3	30.0	4	2	US-10-006-869-144	Sequence 144, App							
159	3	30.0	4	2	US-10-006-869-362	Sequence 362, App							
160	3	30.0	4	2	US-10-006-869-364	Sequence 364, App							
161	3	30.0	4	6	5171670-4	Patent No. 5171670							
162	3	30.0	5	1	US-08-384-618-7	Sequence 7, Appl							
163	3	30.0	5	1	US-08-233-788A-1	Sequence 1, Appl							
164	3	30.0	5	1	US-08-441-591-65	Sequence 65, Appl							
165	3	30.0	5	1	US-08-303-362A-65	Sequence 65, Appl							
166	3	30.0	5	1	US-08-366-783-6	Sequence 6, Appl							
167	3	30.0	5	1	US-08-702-673-1	Sequence 1, Appl							
168	3	30.0	5	1	US-08-598-873-51	Sequence 51, Appl							
169	3	30.0	5	1	US-08-846-021A-9	Sequence 9, Appl							
170	3	30.0	5	1	US-08-423-091C-1	Sequence 1, Appl							
171	3	30.0	5	2	US-08-144-779C-41	Sequence 41, Appl							
172	3	30.0	5	2	US-09-020-880-39	Sequence 39, Appl							
173	3	30.0	5	2	US-09-020-880-41	Sequence 41, Appl							

## ALIGNMENTS

RESULT 1  
PCT-US93-01669-28  
Sequence 28, Application PC/TUS9301669

GENERAL INFORMATION:

APPLICANT: Trowbridge, Ian S.  
APPLICANT: Collawn, Jr., James F.

APPLICANT: Tainer, John A.  
APPLICANT: Kuhn, Leslie A.  
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS  
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESSES:  
ADDRESS: Spensley Horn Ubae & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA

ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01669  
FILING DATE: 01-MAR-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/844,852  
FILING DATE: 03-MAR-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-1636  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
PCT-US93-01669-28

Query Match 50.0%; Score 5; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P00GF 10  
DB 1 P00GF 5

## RESULT 2

PCT-US93-01669-56  
Sequence 56, Application PC/TUS9301669  
GENERAL INFORMATION:  
APPLICANT: Trowbridge, Ian S.  
APPLICANT: Collawn, Jr., James F.  
APPLICANT: Tahner, John A.  
APPLICANT: Kuhn, Leslie A.  
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01669  
FILING DATE: 01-MAR-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/844,852  
FILING DATE: 03-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-1636  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US93-01669-56

Query Match 50.0%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P00GF 10  
DB 3 P00GF 7

## RESULT 3

US-08-785-668-4  
Sequence 4, Application US/08785668  
Patent No. 6265204  
GENERAL INFORMATION:  
APPLICANT: Ward et al.  
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION  
TITLE OF INVENTION: POLYPEPTIDES FOR SECRETION OF FILAMENTOUS

TITLE OF INVENTION: FUNGI  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International, Inc.  
STREET: 925 Page Mill Road  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94304-1013  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/785,668  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/785,668  
FILING DATE: 17-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Stone, Christopher L.  
REGISTRATION NUMBER: 35,696  
REFERENCE/DOCKET NUMBER: GC-284  
TELEPHONE: 650-846-7620  
TELEFAX: 650-846-6504  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-785-668-4

Query Match 40.0%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYL 4  
DB 2 EEYL 5

## RESULT 4

US-09-912-733-4  
Sequence 4, Application US/09912733  
Patent No. 6590078  
GENERAL INFORMATION:  
APPLICANT: Ward, Michael D.  
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF  
FILE REFERENCE: A-62926-1  
CURRENT APPLICATION NUMBER: US/09/912,733  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 08/785,668  
PRIOR FILING DATE: 1997-01-17  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic.

US-09-912-733-4

Query Match 40.0%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYL 4

Db 2 EBYL 5

RESULT 5  
US-09-581-944A-25  
Sequence 25, Application US/09581944A  
Patent No. 6441131

GENERAL INFORMATION:

APPLICANT: Ono Pharmaceutical Co., Ltd.

TITLE OF INVENTION: PEPTIDES, METHOD FOR ASSAYING HUMAN PEPSINOGEN II OR HUMAN PEPSIN

FILE REFERENCE: Q59565

CURRENT APPLICATION NUMBER: US/09/581,944A

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: P. Hei. 9-364796

PRIOR FILING DATE: 1997-12-22

PRIOR APPLICATION NUMBER: P. Hei. 10-213513

PRIOR FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: PCT/JP98/05780

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: substrate for human pepsin II or pepsinogen II

NAME/KEY: MISC\_FEATURE

LOCATION: (5)..(5)

OTHER INFORMATION: 2-naphthyl Ala

NAME/KEY: MISC\_FEATURE

LOCATION: (6)..(6)

OTHER INFORMATION: Ala which binds to p-nitroaniline

US-09-581-944A-25

Query Match 40.0%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PQQ 9  
Db 1 PQQ 4

RESULT 6  
US-09-147-933-19  
Sequence 19, Application US/09147933A  
Patent No. 6168917

GENERAL INFORMATION:

APPLICANT: Kilpatrick, David

TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF

FILE REFERENCE: 62242/US

CURRENT APPLICATION NUMBER: US/09/147,933A

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: PCT/US97/17734

PRIOR FILING DATE: 1997-10-01

PRIOR APPLICATION NUMBER: U. S. 60/027,353

PRIOR FILING DATE: 1996-10-02

NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 19

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: peptide

US-09-147-933-19

Query Match 40.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LVPO 7  
Db 4 LVPO 7

RESULT 7  
US-09-581-944A-20  
Sequence 20, Application US/09581944A  
Patent No. 6441131

GENERAL INFORMATION:

APPLICANT: Ono Pharmaceutical Co., Ltd.

TITLE OF INVENTION: PEPTIDES, METHOD FOR ASSAYING HUMAN PEPSINOGEN II OR HUMAN PEPSIN

FILE REFERENCE: Q59565

CURRENT APPLICATION NUMBER: US/09/581,944A

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: P. Hei. 9-364796

PRIOR FILING DATE: 1997-12-22

PRIOR APPLICATION NUMBER: P. Hei. 10-213513

PRIOR FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: PCT/JP98/05780

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: substrate for human pepsin II or pepsinogen II

NAME/KEY: MISC\_FEATURE

LOCATION: (6)..(6)

OTHER INFORMATION: 4-Iodo-Phenyl Ala

NAME/KEY: MISC\_FEATURE

LOCATION: (7)..(7)

OTHER INFORMATION: Ala which binds to p-nitroaniline

US-09-581-944A-20

Query Match 40.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VPOQ 8  
Db 1 VPOQ 4

RESULT 8  
5422249-15  
Patent No. 5422249

APPLICANT: LIESCH, MANFRED; RINK, HANS; MARKI, WALTER; GRUTTER,

MARKUS G.; MEYHACK, BERND

TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF THROMBIN

NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA: US/08/121,974

FILING DATE: 15-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 700,9978

FILING DATE: 10-MAY-1991

APPLICATION NUMBER: 582,816

FILING DATE: 13-SEP-1990

APPLICATION NUMBER: 211,065

FILING DATE: 20-JUN-1988

APPLICATION NUMBER: 744,453

FILING DATE: 13-JUN-1985



SEQ ID NO:15:  
LENGTH: 7  
5422249-15

Query Match 40.0%; Score 4; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 3 EBYL 6

RESULT 9  
US-08-037-574A-7  
Sequence 7, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-7

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 10

US-08-037-574A-9  
Sequence 9, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-9

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 11  
US-08-037-574A-13  
Sequence 13, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles

STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: described below:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-13

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYVL 4  
DB 5 EYVL 8

RESULT 12  
US-08-037-574A-17  
Sequence 17, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-17

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYVL 4  
DB 5 EYVL 8

RESULT 13  
US-08-037-574A-79  
Sequence 79, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: described below:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS

TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-79

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

## RESULT 14

US-08-037-574A-81  
Sequence 81, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: Including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:

## US-08-037-574A-81

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

## RESULT 15

US-08-037-574A-83  
Sequence 83, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: Including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:

## US-08-037-574A-83

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

## RESULT 16

US-08-037-574A-100  
Sequence 100, Application US/08037574A  
Patent No. 5656600

GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-100

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 17  
US-08-037-574A-106  
Sequence 106, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-106

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 18  
US-08-037-574A-114  
Sequence 114, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-114

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||||  
DB 5 EBYL 8

RESULT 19  
US-08-037-574A-118  
; Sequence 118, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; APPLICANT: THOMAS R. WEBB  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/037,574A  
; FILING DATE: 25 MARCH 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: No. 5656600e  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 200/188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 118:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-037-574A-118

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||||  
DB 5 EBYL 8

RESULT 20  
US-08-037-574A-151  
; Sequence 151, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; APPLICANT: THOMAS R. WEBB  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/037,574A  
; FILING DATE: 25 MARCH 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: No. 5656600e  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 200/188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 151:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-037-574A-151

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||||  
DB 5 EBYL 8

RESULT 21  
US-08-037-574A-157  
; Sequence 157, Application US/08037574A  
; Patent No. 5656600  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
; APPLICANT: PEASON, GEORGE P. VLASUK,  
; APPLICANT: THOMAS R. WEBB  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS

TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 157:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-157

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 22  
US-08-037-574A-163  
Sequence 163, Application US/08037574A  
Patent No. 5656600  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, DANIEL A.  
APPLICANT: PEASON, GEORGE P. VLASUK,  
APPLICANT: THOMAS R. WEBB  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/037,574A  
FILING DATE: 25 MARCH 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 5656600e  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 200/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-037-574A-163

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 23  
US-08-218-329-7  
Sequence 7, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 24  
US-08-218-329-9  
Sequence 9, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:

US-08-218-329-9  
Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 25  
US-08-218-329-13  
Sequence 13, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:

US-08-218-329-13  
Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 26  
US-08-218-329-17  
Sequence 17, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-17

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 27  
US-08-218-329-79  
Sequence 79, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-79

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8

RESULT 28  
US-08-218-329-81  
Sequence 81, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
TITLE OF INVENTION: INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-81

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 5 EBYL 8



RESULT 29  
US-08-218-329-83  
Sequence 83, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-83

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
DB 5 EBYL 8

RESULT 30  
US-08-218-329-99  
Sequence 99, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-99

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
DB 5 EBYL 8

RESULT 31  
US-08-218-329-105  
Sequence 105, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 105:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-218-329-105

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 32  
US-08-218-329-113  
; Sequence 113, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,329  
; FILING DATE: 25-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/037,574  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 206/222  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-218-329-113

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
,Db 5 EBYL 8

RESULT 33  
US-08-218-329-117  
; Sequence 117, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,329  
; FILING DATE: 25-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/037,574  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, Suzanne L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 206/222  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-08-218-329-117

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
|||  
Db 5 EBYL 8

RESULT 34  
US-08-218-329-150  
; Sequence 150, Application US/08218329  
; Patent No. 5670479  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW M. ABELMAN, ET AL.  
; TITLE OF INVENTION: ALPHA-KETAMIDE DERIVATIVES AS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-150

Query Match  
Best local Similarity 40.0%; Score 4; DB 1; Length 8;  
Matches 4; Conservativity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;

QY 1 BEYL 4  
|||  
DB 5 BEYL 8

RESULT 35  
US-08-218-329-156  
Sequence 156, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-156

Query Match  
Best local Similarity 40.0%; Score 4; DB 1; Length 8;  
Matches 4; Conservativity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;

QY 1 BEYL 4  
|||  
DB 5 BEYL 8

RESULT 36  
US-08-218-329-162  
Sequence 162, Application US/08218329  
Patent No. 5670479  
GENERAL INFORMATION:  
APPLICANT: MATTHEW M. ABELMAN, ET AL.  
TITLE OF INVENTION: ALPHA-KETOAMIDE DERIVATIVES AS  
INHIBITORS OF THROMBOSIS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/218,329  
FILING DATE: 25-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,574  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, Suzanne L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 206/222  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-08-218-329-162

Query Match  
Best local Similarity 40.0%; Score 4; DB 1; Length 8;  
Matches 4; Conservativity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;

QY 1 BEYL 4  
|||

Db 5 EBYL 8

RESULT 37

US-08-482-228-137  
Sequence 137, Application US/08482228  
Patent No. 5968753

GENERAL INFORMATION:

APPLICANT: Teeng-Law, Janet

APPLICANT: Kobori, Joan A.

APPLICANT: Al-Abdaly, Fahad A.

APPLICANT: Guillermo, Roy

APPLICANT: Helgeson, Sam L.

APPLICANT: Deans, Robert J.

TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL

SELECTION MEDIATED BY PEPTIDE RELEASE

NUMBER OF SEQUENCES: 215

CORRESPONDENCE ADDRESS:

ADDRESSER: Janice Guthrie, Ph.D.

STREET: P.O. Box 15210

CITY: Irvine

STATE: California

COUNTRY: USA

ZIP: 92713-5210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,228

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Guthrie, Janice

REGISTRATION NUMBER: 35,170

REFERENCE/DOCKET NUMBER: IT-4630CIP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 440-5353

TELEFAX: (714) 553-1952

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-482-228-137

Query Match 40.0%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 7 QOGF 10  
Db 1 QOGF 4RESULT 38  
US-08-482-528-137

Sequence 137, Application US/0848528

Patent No. 6017719

GENERAL INFORMATION:

APPLICANT: Teeng-Law, Janet

APPLICANT: Kobori, Joan A.

APPLICANT: Al-Abdaly, Fahad A.

APPLICANT: Guillermo, Roy

APPLICANT: Helgeson, Sam L.

APPLICANT: Deans, Robert J.

TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL

SELECTION MEDIATED BY PEPTIDE RELEASE

NUMBER OF SEQUENCES: 215

CORRESPONDENCE ADDRESS:

ADDRESSER: Janice Guthrie, Ph.D.

STREET: P.O. Box 15210

CITY: Irvine

STATE: California

COUNTRY: USA

ZIP: 92713-5210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,528

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Guthrie, Janice

REGISTRATION NUMBER: 35,170

REFERENCE/DOCKET NUMBER: IT-4630CIP4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 440-5353

TELEFAX: (714) 553-1952

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-482-528-137

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 7 QOGF 10  
Db 1 QOGF 4RESULT 39  
US-09-239-043D-198

Sequence 198, Application US/09239043D

Patent No. 6689363

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Vitiello, Maria A.

APPLICANT: Livingston, Brian D.

APPLICANT: Cells, Euseban

APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.

APPLICANT: Cheesnut, Robert

APPLICANT: Epiimmune Inc.

TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

SELECTION MEDIATED BY Nucleic Acid Compositions

FILE REFERENCE: 2060.0060007

CURRENT APPLICATION NUMBER: US/09/239,043D

FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/978,291

PRIOR FILING DATE: 1997-11-25

PRIOR APPLICATION NUMBER: US 08/820,360

PRIOR FILING DATE: 1997-03-12

PRIOR APPLICATION NUMBER: US 60/013,363

PRIOR FILING DATE: 1996-03-13

PRIOR APPLICATION NUMBER: US 08/461,603

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01

PRIOR APPLICATION NUMBER: US 08/344,824

PRIOR FILING DATE: 1994-11-23

PRIOR APPLICATION NUMBER: US 08/278,634

PRIOR FILING DATE: 1994-07-21  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/197,484  
PRIOR FILING DATE: 1994-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2579  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 198  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Orthohepadnaviridae hepatitis B virus  
US-09-239-043D-198

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYLV 5  
Db 5 EYLV 8

RESULT 40  
US-09-239-043D-1346  
Sequence 1346, Application US/09239043D  
Patent No. 6689363  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Vitello, Maria A.  
APPLICANT: Livingston, Brian D.  
APPLICANT: Cells, Esteban  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Chesnut, Robert  
APPLICANT: Eptimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus  
FILE REFERENCE: 2060.0060007  
CURRENT APPLICATION NUMBER: US/09/239,043D  
CURRENT FILING DATE: 1999-01-27  
PRIOR APPLICATION NUMBER: US 09/189,702  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 08/978,291  
PRIOR FILING DATE: 1997-11-25  
PRIOR APPLICATION NUMBER: US 08/820,360  
PRIOR FILING DATE: 1997-03-12  
PRIOR APPLICATION NUMBER: US 60/013,363  
PRIOR FILING DATE: 1996-03-13  
PRIOR APPLICATION NUMBER: US 08/461,603  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
PRIOR APPLICATION NUMBER: US 08/344,824  
PRIOR FILING DATE: 1994-11-23  
PRIOR APPLICATION NUMBER: US 08/278,634  
PRIOR FILING DATE: 1994-07-21  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/197,484  
PRIOR FILING DATE: 1994-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2579  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1346  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Orthohepadnaviridae hepatitis B virus  
US-09-239-043D-1346  
Query Match 40.0%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYLV 5  
Db 5 EYLV 8

RESULT 41  
5196404-2  
Patent No. 5196404  
APPLICANT: MARGANORE, JOHN M., FENTON II, JOHN M., KLINE, TONI  
TITLE OF INVENTION: INHIBITORS OF THROMBIN  
NUMBER OF SEQUENCES: 18  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/549,388  
FILING DATE: 06-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 395,482  
FILING DATE: 18-AUG-1989  
SEQ ID NO: 2  
LENGTH: 8  
5196404-2

Query Match 40.0%; Score 4; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLV 4  
Db 5 EYLV 8

RESULT 42  
US-08-467-083-23  
Sequence 23, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 43  
US-08-414-417B-23

Sequence 23, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:

ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,417B

FILING DATE: 31-MAR-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-414-417B-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 44

US-08-486-348A-23

Sequence 23, Application US/08486348A

Patent No. 5846538

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,348A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-486-348A-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYL 4  
|||  
DB 6 EBYL 9

RESULT 45

US-08-468-545B-23

Sequence 23, Application US/08468545B

Patent No. 5876712

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,545B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-466-545B-23

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
Db 6 EBYL 9

RESULT 46  
US-08-466-680B-23  
Sequence 23, Application US/08466680B

PATENT INFORMATION:  
PATENT NO. 6075122  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-466-680B-23

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
Db 6 EBYL 9

RESULT 47  
US-09-692-170C-40  
Sequence 40, Application US/09692170C  
Patent No. 6562345  
GENERAL INFORMATION:

APPLICANT: Diamond, Don J.  
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS  
FILE REFERENCE: 1954-346  
CURRENT APPLICATION NUMBER: US/09/692,170C  
CURRENT FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 09/534,639  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 09/075,257  
PRIOR FILING DATE: 1998-05-11  
PRIOR APPLICATION NUMBER: US 09/021,298  
PRIOR FILING DATE: 1998-02-10  
PRIOR APPLICATION NUMBER: US 08/950,064  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: US 08/747,488  
PRIOR FILING DATE: 1996-11-12  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 40  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Amidated variant human cytomegalovirus peptide epitope  
NAME/KEY: MOD\_RSS  
LOCATION: (9)-(9)  
OTHER INFORMATION: AMIDATION  
US-09-692-170C-40

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6  
Db 1 YLVP 4

RESULT 48  
US-09-692-170C-41  
Sequence 41, Application US/09692170C  
Patent No. 6562345

GENERAL INFORMATION:  
APPLICANT: Diamond, Don J.  
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS  
FILE REFERENCE: 1954-346  
CURRENT APPLICATION NUMBER: US/09/692,170C  
CURRENT FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 09/534,639  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 09/075,257  
PRIOR FILING DATE: 1998-05-11  
PRIOR APPLICATION NUMBER: US 09/021,298  
PRIOR FILING DATE: 1998-02-10  
PRIOR APPLICATION NUMBER: US 08/950,064  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: US 08/747,488  
PRIOR FILING DATE: 1996-11-12  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 41  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Amidated variant human cytomegalovirus peptide epitope  
NAME/KEY: MOD\_RSS  
LOCATION: (9)-(9)  
OTHER INFORMATION: AMIDATION  
US-09-692-170C-41

Query Match 40.0%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YLVP 4

Search completed: January 18, 2006, 21:07:29  
Job time : 46 secs

QY 3 YLVP 6  
1 YLVP 4

RESULT 49

US-09-692-325-37  
; Sequence 37, Application US/09692325  
; Patent No. 6632435  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Don  
; TITLE OF INVENTION: CTL Epitope Analogs  
; FILE REFERENCE: 1954-314  
; CURRENT APPLICATION NUMBER: US/09/692,325  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/160633  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: US 60/187871  
; PRIOR FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCMV vaccine peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: AMIDATION  
US-09-692-325-37

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6  
1 YLVP 4

RESULT 50

US-09-692-325-38  
; Sequence 38, Application US/09692325  
; Patent No. 6632435  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Don  
; TITLE OF INVENTION: CTL Epitope Analogs  
; FILE REFERENCE: 1954-314  
; CURRENT APPLICATION NUMBER: US/09/692,325  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/160633  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: US 60/187871  
; PRIOR FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCMV vaccine peptide  
US-09-692-325-38

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:56:58 ; Search time 157 Seconds  
(without alignments)  
44.938 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 10

Sequence: 1 BEYLVPGQGF 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3063

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database : UniProt 05.80:\*

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	7	1	PAP2_ASCSU
2	3	30.0	7	1	PAP2_PANRE
3	3	30.0	8	1	LCK3_LEUMA
4	3	30.0	8	1	PPK3_PERAM
5	3	30.0	8	2	Q83332_GCCRO
6	3	30.0	9	1	PAP1_CALVO
7	3	30.0	9	1	UPAT_HUMAN
8	3	30.0	9	2	P78484_HUMAN
9	3	30.0	10	1	GPCR_MOUSE
10	3	30.0	10	2	Q8WGD2_9EUCU
11	3	30.0	10	2	Q7MIF6_9POAL
12	3	30.0	10	2	Q7MIF7_9POAL
13	3	30.0	10	2	Q8L7E5_HEYBR
14	3	30.0	10	2	Q53VQ3_MOUSE
15	3	30.0	10	2	Q53VQ7_MOUSE
16	3	30.0	10	2	Q53VRI_MOUSE
17	3	30.0	10	2	Q83978_9INPA
18	2	20.0	4	1	ACR1_ACFPU
19	2	20.0	4	1	PAP3_HIRME
20	2	20.0	4	1	OCPI_OCTMI
21	2	20.0	5	1	PAP2_PARMA
22	2	20.0	5	1	PRCT_CARMA
23	2	20.0	5	1	PRCT_LIMPO
24	2	20.0	5	1	PRCT_PERAM
25	2	20.0	5	1	RB332_LITRU
26	2	20.0	5	1	TRAM3_ECOLI
27	2	20.0	6	1	ASP2_LACSN
28	2	20.0	6	1	E101_LITRU
29	2	20.0	7	1	ASCL_ALIAS
30	2	20.0	7	1	CAP6_CANAL
31	2	20.0	7	1	CCP1_BMTFA

32	2	20.0	7	1	TPPY_PACDA
33	2	20.0	7	1	UF03_MOUSE
34	2	20.0	7	1	UH11_RAT
35	2	20.0	7	2	Q8NHH7_HUMAN
36	2	20.0	7	2	Q8NHH7_HUMAN
37	2	20.0	7	2	Q8NHH7_HUMAN
38	2	20.0	7	2	Q8NHH7_HUMAN
39	2	20.0	7	2	Q8NHH7_HUMAN
40	2	20.0	7	2	Q8NHH7_HUMAN
41	2	20.0	7	2	Q8NHH7_HUMAN
42	2	20.0	7	2	Q8NHH7_HUMAN
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75	2	20.0	7	2	Q8NHH7_HUMAN
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77	2	20.0	7	2	Q8NHH7_HUMAN
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104	2	20.0	7	2	Q8NHH7_HUMAN

105	2	20.0	8	2	Q9T2Y3_9ROSI	Q9C2Y3 begonia for
106	2	20.0	8	2	Q9T2M4_9ROSI	Q9C2M4 begonia for
107	2	20.0	8	2	Q9XG18_9ROSI	Q9XG18 begonia chi
108	2	20.0	8	2	Q9XG15_9ROSI	Q9XG15 begonia nan
109	2	20.0	8	2	Q6Z201_SITCR	Q6Z201 silene conti
110	2	20.0	8	2	Q56140_STCTR	Q56140 streptococc
111	2	20.0	8	2	P83532_LACSN	P83532 lactobacill
112	2	20.0	8	2	Q79C66_MYXXA	Q79C66 myxococcus
113	2	20.0	8	2	Q7X405_NODSP	Q7X405 nodularia s
114	2	20.0	8	2	Q9R4M3_ENTFA	Q9R4M3 enterococcu
115	2	20.0	8	2	Q9RQ43_9ENTR	Q9RQ43 buchnera ap
116	2	20.0	8	2	Q9RQ57_9ENTR	Q9RQ57 buchnera ap
117	2	20.0	8	2	Q9X3K1_9PROC	Q9X3K1 pichlorococ
118	2	20.0	8	2	Q56429_THETH	Q56429 thermus the
119	2	20.0	8	2	Q78D66_RAT	Q78D66 rattus norv
120	2	20.0	8	2	Q7M032_RAT	Q7M032 rattus norv
121	2	20.0	8	2	Q7M039_RAT	Q7M039 rattus norv
122	2	20.0	8	2	Q7M041_RAT	Q7M041 rattus norv
123	2	20.0	8	2	Q8CJ03_MOUSE	Q8CJ03 mus musculu
124	2	20.0	8	2	Q99P40_MOUSE	Q99P40 mus musculu
125	2	20.0	8	2	Q9RT21_MOUSE	Q9RT21 mus musculu
126	2	20.0	8	2	Q9RT16_MOUSE	Q9RT16 mus musculu
127	2	20.0	8	2	Q6Z527_MOSSP	Q6Z527 mus spretus
128	2	20.0	8	2	Q83977_9INFA	Q83977 influenza a
129	2	20.0	8	2	Q83349_9COCO	Q83349 murine hepa
130	2	20.0	8	2	Q89498_9COCO	Q89498 murine hepa
131	2	20.0	8	2	Q5Y8D4_ONCMY	Q5Y8D4 oncofynchu
132	2	20.0	8	2	Q681P1_9PASS	Q681P1 mymocheul
133	2	20.0	8	2	Q68LQ3_9PASS	Q68LQ3 bakesphorus
134	2	20.0	8	2	Q6R7U6_9SAUR	Q6R7U6 gnyptescocin
135	2	20.0	8	2	Q8UJ35_9PASS	Q8UJ35 filicula hy
136	2	20.0	8	2	Q90ZV5_9GRUI	Q90ZV5 flicula leuc
137	2	20.0	8	2	Q94V82_9SAUR	Q94V82 varanus yuw
138	2	20.0	8	2	Q94VA7_9SAUR	Q94VA7 varanus yuw
139	2	20.0	8	2	Q94VB2_9SAUR	Q94VB2 varanus sal
140	2	20.0	8	2	Q94VB5_9SAUR	Q94VB5 varanus sal
141	2	20.0	9	1	ALU10_CARMA	P81813 carcinus ma
142	2	20.0	9	1	BRI1_RANMI	Q71254 rana nigrom
143	2	20.0	9	1	CAER_PHYSA	Q71AC4 phyllomedus
144	2	20.0	9	1	CR82_SPTOL	Q9C2K9 spinacia ol
145	2	20.0	9	1	CK6A1_THROB	P80975 thunnus obe
146	2	20.0	9	1	PARS_PANRE	P82661 panagrellus
147	2	20.0	9	1	FARD_CALVO	P19946 calliphora
148	2	20.0	9	1	FIBB_EERYA	P41846 erythrocebu
149	2	20.0	9	1	FIBB_MACFU	P19345 macaca fusc
150	2	20.0	9	1	FLA42_TREHY	P80159 treponema h
151	2	20.0	9	1	KNT3_BOMVA	P83058 bombina var
152	2	20.0	9	1	KNT3_CYPDO	P83659 cyphononyx
153	2	20.0	9	1	LITO_LITAO	P08945 litorea aur
154	2	20.0	9	1	LMT3_LOCM1	P41489 locusta mig
155	2	20.0	9	1	OXYT_RAJICL	P42394 raja clavac
156	2	20.0	9	1	PKR1_PERAM	P82691 periplaneta
157	2	20.0	9	1	PVK2_SARBU	P84353 sarcophaga
158	2	20.0	9	1	RHG_RAT	P84107 rattus norv
159	2	20.0	9	1	SNMF_MOSCA	P19095 muscelus ca
160	2	20.0	9	1	THYF_PIG	P01255 sus scrofa
161	2	20.0	9	1	TKL1_LOCM1	P16223 locusta mig
162	2	20.0	9	1	TRP4_LEUMA	P81736 leucophaea
163	2	20.0	9	1	UHA2_HUMAN	P40629 homo sapien
164	2	20.0	9	1	ULAD_HUMAN	P31929 homo sapien
165	2	20.0	9	1	ULAH_HUMAN	P31934 homo sapien
166	2	20.0	9	2	Q7RY89_NEUCR	Q7RY89 neurospora
167	2	20.0	9	2	Q7S182_NEUCR	Q7S182 neurospora
168	2	20.0	9	2	Q9P885_KLITA	Q9P885 kluyveromyc
169	2	20.0	9	2	Q9S953_HUMAN	Q9S953 homo sapien
170	2	20.0	9	2	Q16220_HUMAN	Q16220 homo sapien
171	2	20.0	9	2	Q5QEX9_HUMAN	Q5QEX9 homo sapien
172	2	20.0	9	2	Q67AO7_HUMAN	Q67AO7 homo sapien
173	2	20.0	9	2	Q67AR4_HUMAN	Q67AR4 homo sapien
174	2	20.0	9	2	Q67AR6_HUMAN	Q67AR6 homo sapien
175	2	20.0	9	2	Q67AR7_HUMAN	Q67AR7 homo sapien
176	2	20.0	9	2	Q67AT1_HUMAN	Q67AT1 homo sapien
177	2	20.0	9	2	Q67AT2_HUMAN	Q67AT2 homo sapien

178	2	20.0	9	2	Q71EB9_HUMAN	Q71EB9 homo sapien
179	2	20.0	9	2	Q81UJ5_HUMAN	Q81UJ5 homo sapien
180	2	20.0	9	2	Q99887_HUMAN	Q99887 homo sapien
181	2	20.0	9	2	Q9UCN5_HUMAN	Q9UCN5 homo sapien
182	2	20.0	9	2	Q9UCQ9_HUMAN	Q9UCQ9 homo sapien
183	2	20.0	9	2	Q9UCS8_HUMAN	Q9UCS8 homo sapien
184	2	20.0	9	2	Q9UK44_HUMAN	Q9UK44 homo sapien
185	2	20.0	9	2	Q53VS2_HUMAN	Q53VS2 homo sapien
186	2	20.0	9	2	Q9UMF3_HUMAN	Q9UMF3 homo sapien
187	2	20.0	9	2	Q4PIZ7_HUMAN	Q4PIZ7 homo sapien
188	2	20.0	9	2	P92072_PPTUM	P92072 euhadra her
189	2	20.0	9	2	Q7M3J3_PENVA	Q7M3J3 penaeus van
190	2	20.0	9	2	Q7M471_VESOR	Q7M471 vespa orien
191	2	20.0	9	2	Q8WS88_ANTCR	Q8WS88 antiochidari
192	2	20.0	9	2	Q9TW66_LEPDE	Q9TW66 leptinotars
193	2	20.0	9	2	Q9TWX7_MANSE	Q9TWX7 manduca sex
194	2	20.0	9	2	Q7RCJ3_PLAYO	Q7RCJ3 plasmodium
195	2	20.0	9	2	Q8WBW5_DIASZ	Q8WBW5 diadema set
196	2	20.0	9	2	Q8WBW6_SECHN	Q8WBW6 diadema ant
197	2	20.0	9	2	Q8WBX4_SECHN	Q8WBX4 diadema mex
198	2	20.0	9	2	Q8WFS4_SECHN	Q8WFS4 diadema mex
199	2	20.0	9	2	Q8WFT3_SECHN	Q8WFT3 diadema ant
200	2	20.0	9	2	Q4Y9N3_PLABE	Q4Y9N3 plasmodium

## ALIGNMENTS

## RESULT 1

PF2\_ASCSU STANDARD, PRT: 7 AA.

AC PF2\_7879; P31890; PubMed=8332542; DOI=10.1016/0196-9781(93)90127-3;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Peptide-like neuropeptide AP2.  
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoideae).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
 CC Ascaridoidea; Ascaridae.  
 OX NCBI\_TaxId=6253;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93324431; PubMed=8332542; DOI=10.1016/0196-9781(93)90127-3;  
 RA Cowden C., Stretton A.O.W.;  
 RT "AP2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";  
 RL Peptides 14:423-430(1993).  
 CC -|- FUNCTION: Has effects on muscle tension.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.  
 CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Amiation; Direct protein sequencing; Neuropeptide.  
 KW MOD RES 7 Phenylalanine amide.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B1B350 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.2e+06; Mismatches 0; Gaps 0;

Matches 3; Conservative 0; Indels 0;

QY 2 EYL 4

DB 3 EYL 5

RESULT 2

FAF2\_PANRE STANDARD; PRT; 7 AA.

AC P67860; P31890; (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE FMRamide-like neuropeptide AF2.

OS Pangrelus redivivus.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

OC Pangrolaimidae; Pangrolaimidae; Pangrelus.

OX NCBI\_TaxId=6233;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=95060998; PubMed=7970891;

RA Maule A.G., Shaw C., Bowman J.W.;

RT "The FMRamide-like neuropeptide AF2 (Ascaris suum) is present in the free-living nematode, Pangrelus redivivus (Nematoda, Rhabditida)."; Parasitology 109:351-356(1994).

RL Parascitology 109:351-356(1994).

CC -1- FUNCTION: Has effects on muscle tension.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.

CC -1- SIMILARITY: Belongs to the FAPR (FMRamide related peptide) family.

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KM Amidation; Direct protein sequencing; Neuropeptide.

FT MOD RES 7 Phenylalanine amide.

FT SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

SO

Query Match 30.0%; Score 3; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 EYL 4

Db 3 EYL 5

-----

RESULT 3

LCK3\_LEUMA STANDARD; PRT; 8 AA.

ID LCK3 LEUMA (Rel. 18, Created)

AC P21142;

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Leucokinin-3 (leucokinin III) (L-III).

OS Leucophaea maderae (Maderia cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberodea;

OC Blaberidae; Leucophaea.

OX NCBI\_TaxId=6988;

RN [1]

RP PROTEIN SEQUENCE, AND SYNTHESIS.

RT TISSUE=Head;

RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotopsins.";

RL Comp. Biochem. Physiol. 84C:271-276(1986).

CC -1- FUNCTION: This cephalomyotopic peptide stimulates contractile activity of cockroach prolegum (hindgut).

CC -1- SUBCELLULAR LOCATION: Secreted.

-----

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CC Amidation; Direct protein sequencing; Neuropeptide.

KM MOD RES 8 Glycine amide.

FT SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

SO

Query Match 30.0%; Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 OGF 10

Db 2 OGF 4

-----

RESULT 4

PPK3\_PPRAM STANDARD; PRT; 8 AA.

ID PPK3\_PPRAM (Rel. 40, Created)

AC P82618;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Pyrokinin-3 (pea-PK-3) (FXPRL-amide).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatodea;

OC Blattidae; Blattinae; Periplaneta.

OX NCBI\_TaxId=6978;

RN [1]

RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Retrocerebral complex;

RX MEDLINE=99212469; PubMed=10196736; DOI=10.1016/S0965-1748(98)00117-9;

RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;

RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neuromal organs of the American cockroach.";

RL Insect Biochem. Mol. Biol. 29:139-144(1999).

RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=20189894; PubMed=10723010;

RA Predel R., Eckert M.;

RT "Tagma-specific distribution of FXPRlamides in the nervous system of the American cockroach.";

RL J. Comp. Neurol. 419:352-363(2000).

CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic activity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Corpora cardiaca.

CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI; RANGE=1-8; NOTE=Ref.1.

CC -1- SIMILARITY: Belongs to the pyrokinin family.

-----

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DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ; FALSE NEG.

KM Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.

FT MOD RES 8 Leucine amide.

FT SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

SO

Query Match 30.0%; Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LVP 6

Db 1 LVP 3

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RESULT 5

083332\_9CORO PRELIMINARY; PRT; 8 AA.

ID 083332\_9CORO PRELIMINARY;

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AC Q83332;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HE (Fragment).
OS Murine hepatitis virus.
CC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
CC Coronaviridae; Coronavirus; Group 2 species.
CX NCBI_TaxID=11138;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JHM;
RX MEDLINE=95191005; PubMed=7884877;
RA Kim K.H., Makino S.;
RT "Two murine coronavirus genes suffice for viral RNA synthesis.";
RL J. Virol. 69:2313-2321(1995).
DR EMBL; U19933; AAA69002.1; -; Genomic_RNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 907 MW; 922735B1735A2CD CRC64;

Query Match 30.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYL 4
DB 5 EYL 7

RESULT 6
FRL CALVO STANDARD; PRT; 9 AA.
ID P41856;
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CalliFMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Calliphoridae; Calliphora.
CX NCBI_TaxID=27454;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RT Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly Calliphora
RT vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the PARP (FMRamide related peptide)
CC family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A41978; A41978.
KW Amidation; Direct protease sequencing; Neuropeptide.
FT MOD_RES 9 Phenylalanine amide.
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 PQQ 8
DB 2 PQQ 4

RESULT 7
UPA7 HUMAN STANDARD; PRT; 9 AA.
ID UPA7 HUMAN
AC P30093;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Unknown protein from 2D-PAGE of plasma (Spot 18) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquall C.,
RA Sanchez J.-C., James R., Tisot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.05, its MW is: 37 kDa.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC SWISS-2DPAGE; P30093; HUMAN.
DR Direct protein sequencing.
FT UNSURE
FT NON_TER
FT NON_TER
SQ SEQUENCE 9 AA; 1043 MW; SC14477AEB0772C7 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6
DB 2 LVP 4

RESULT 8
P78484 HUMAN PRELIMINARY; PRT; 9 AA.
ID P78484;
AC P78484;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE FYN protein (Fragment).
GN Name=FYN;
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88234523; PubMed=3287380;
RA Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;
RT "Acquisition of transforming properties by FYN, a normal SRC-related
RT human gene.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874 (1988).  
 DR EMBL; M20284; AAA52491.1; -, Genomic\_DNA.  
 FT NON TER 1 1143 MW; 12BA11729D5A6D73B CRC64;  
 SQ SEQUENCE 9 AA; 1143 MW; 12BA11729D5A6D73B CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYL 4  
 |||  
 Db 1 EYL 3

## RESULT 9

GPCR\_MOUSE STANDARD; PRT; 10 AA.  
 ID GPCR\_MOUSE P83654;  
 AC P83654;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Putative G-protein coupled receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Theria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Testis;  
 RA Laloraya M., Kumar G.P.;  
 RT "Identification of a G-protein coupled receptor (GPCR) on mouse  
 spermatoczoa";  
 RL Submitted (MAR-2004) to Swiss-Prot.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 CC removed.

CC InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR PROSITE; PS00237; G\_PROTEIN\_REC\_P1.1, PARTIAL.  
 DR PROSITE; PS0262; G\_PROTEIN\_REC\_P1.2, PARTIAL.  
 KW Direct protein sequencing; G-protein coupled receptor; Receptor;  
 KW Transducer; Transmembrane.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1192 MW; DBSC8D96944B06C6 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PQQ 8  
 |||  
 Db 2 PQQ 4

## RESULT 10

Q8WGD2\_9EUCA PRELIMINARY; PRT; 10 AA.  
 ID Q8WGD2\_9EUCA PRELIMINARY;  
 AC Q8WGD2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 OS Hepaticus epheliticus (Callio box crab).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Brachyura; Leucostoidae; Calappidae; Hepatus.

OX NCBI\_TaxID=6799;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RT "Mitochondrial gene rearrangements confirm the parallel evolution of  
 RT the crab-like form";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350 (2002).  
 DR EMBL; AF36043; ABJ1618.1; -, Genomic\_DNA.  
 DR GO; GO:0005733; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1178 MW; DB16025452C05B02 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YLV 5  
 |||  
 Db 8 YLV 10

## RESULT 11

Q7M1F6\_9POAL PRELIMINARY; PRT; 10 AA.  
 ID Q7M1F6\_9POAL PRELIMINARY;  
 AC Q7M1F6;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alpha-glucanase 6Ha (Fragment).  
 OS Haynaldia villosa.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Haynaldia.  
 NCBI\_TaxID=40247;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=91315394; PubMed=1859356;  
 RA Shewry P.R., Sebelius P.A., Farmer S., Lafandra D.;  
 RT "Alpha-type prolamin are encoded by genes on chromosomes 4Ha and 6Ha  
 RT of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).";  
 RL Biochem. Genet. 29:207-211 (1991).  
 DR PIR; B61218; B61218.  
 FT NON TER 1  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1132 MW; DEAE5936C772D772 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPQ 7  
 |||  
 Db 5 VPQ 7

## RESULT 12

Q7M1F7\_9POAL PRELIMINARY; PRT; 10 AA.  
 ID Q7M1F7\_9POAL PRELIMINARY;  
 AC Q7M1F7;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alpha-glucanase 4Ha (Fragment).  
 OS Haynaldia villosa.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Haynaldia.  
 NCBI\_TaxID=40247;  
 RN [1]  
 RP PROTEIN SEQUENCE.

RX MEDLINE=9135394; PubMed=1859356;  
 RA Shewry P.R., Sabelli P.A., Parmar S., Iafandra D.;  
 RT "alpha-type prolamin are encoded by genes on chromosomes 4He and 6Ha  
 of *Haynaldia villosa* Schur (syn. *Dasypyrum villosum* L.).",  
 RL Biochem. Genet. 29:207-211(1991).  
 DR PIR: A61218; A61218.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1162 MW; 72F11BC772D772D4 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VPO 7  
 DB 6 VPO 8

RESULT 13  
 OBL7F5 HEVR PRELIMINARY; PRT; 10 AA.  
 ID OBL7F5;  
 AC OBL7F5;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Rubber elongation factor (Fragment).  
 OS Name:ref;  
 OS *Hevea brasiliensis* (Para rubber tree).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Hevea.  
 OC NCBI\_Taxid=3991;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Arcizet P., Jones H.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY134670; FAF95706.1; -; Genomic DNA.  
 DR GO: GO:0003746; Fctranslation elongation factor activity; IEA.  
 KW Elongation factor.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1136 MW; 793CFPD44AAB1AAB CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 QOG 9  
 DB 8 QOG 10

RESULT 14  
 O53VQ3 MOUSE PRELIMINARY; PRT; 10 AA.  
 ID O53VQ3;  
 AC O53VQ3;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE D region (Fragment).  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
 RT "The idotypic network and the internal image: possible regulation of  
 a germ-line network by paucigene encoded Ab2 (anti-idotypic)  
 antibodies in the GAT system.";

RL EMO J. 4:3681-3688(1985).  
 DR EMBL: X03378; CAA27099.1; -; mRNA.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1410 MW; 08620B1AB841B4B CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBY 3  
 DB 8 EBY 10

RESULT 15  
 O53VQ7 MOUSE PRELIMINARY; PRT; 10 AA.  
 ID O53VQ7;  
 AC O53VQ7;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE D region (Fragment).  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
 RT "The idotypic network and the internal image: possible regulation of  
 antibodies in the GAT system.";

RL EMO J. 4:3681-3688(1985).  
 DR EMBL: X03377; CAA27093.1; -; mRNA.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1394 MW; 08620B1AA9D41B4B CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBY 3  
 DB 8 EBY 10

RESULT 16  
 O53VRI MOUSE PRELIMINARY; PRT; 10 AA.  
 ID O53VRI;  
 AC O53VRI;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE D region (Fragment).  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86136012; PubMed=3937730;  
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
 RT "The idotypic network and the internal image: possible regulation of  
 a germ-line network by paucigene encoded Ab2 (anti-idotypic)  
 antibodies in the GAT system.";

FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1368 MW; 08620B1AA1F409DB CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 BEY 3  
 |||  
 DB 8 BEY 10  
 RESULT 17  
 083978\_91NFA PRELIMINARY; PRT; 10 AA.  
 ID 083978\_91NFA  
 AC 083978\_91  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Influenza A/udorn/72 (h3n2), nucleoprotein (seg 5), 3' cDNA.  
 DE (Fragment).  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=11320;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=83112211; PubMed=6296449;  
 RA Lin B.-C., Lai C.-J.;  
 RT "The influenza virus nucleoprotein synthesized from cloned DNA in a  
 RT simian virus 40 vector is detected in the nucleus."  
 RL J. Virol. 45:434-438(1983).  
 DR EMBL: J02171; AAA43463.1; -; Genomic RNA.  
 KW GO: 0030529; C:ribonucleoprotein complex; IEA.  
 DR Ribonucleoprotein; Viral nucleoprotein.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1173 MW; 8787655B1B1DD4A CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 BEY 3  
 |||  
 DB 6 BEY 8  
 RESULT 18  
 ACH1\_ACHFU STANDARD; PRT; 4 AA.  
 ID ACH1\_ACHFU  
 AC P35974;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Achatina-I.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigambrellidae; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP PROTEIN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN=Perussac; TISSUE=Ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Novales B.T., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
 RA Novales B.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica, Perussac containing a D-amino acid residue."  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;

RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function."  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Iehida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
 RT phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
 RT residue."  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
 CC and produces a spike broadening of the identified heart excitatory  
 CC neuron (PON); also enhances the amplitude and frequency of the  
 CC heart beat. Has also an effect on several other muscles.  
 CC -----  
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 CC removed.  
 CC -----  
 CC PIR: A32480; A32480.  
 DR D-amino acid; Direct protein sequencing; Hormone.  
 KW MOD RES 2 D-phenylalanine.  
 FT MOD RES 2  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 GF 10  
 ||  
 DB 1 GF 2  
 RESULT 19  
 PAR3\_HIRME STANDARD; PRT; 4 AA.  
 ID PAR3\_HIRME  
 AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide-like neuropeptide YLRP-amide.  
 OS Hirudo medicinalis (Medical leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
 RA Evans B.D., Pohl J., Karstons M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the PARP (FMRFamide related peptide)  
 CC family.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Annotation: Direct protein sequencing; Neuropeptide.  
 KM MOD RES 4 Phenylalanine amide.  
 FT MOD RES 4  
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YL 4  
DB 1 YL 2

RESULT 20

OCPL OCTMT STANDARD; PRT; 4 AA.

AC P58648;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cardioactive peptides Ocp-1/Ocp-2.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxId=89766;

PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
[1]  
RT TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor.";  
RT Peptides 21:623-630(2000).  
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-2 is a 1000 time less active  
CC than Ocp-1.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.  
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
CC -----  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC D-amino acid; Direct protein sequencing; Hormone.  
KW MOD RES 2 D-phenylalanine (in form Ocp-1).  
FT SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GF 10  
DB 1 GF 2

RESULT 21

PAP2 PARMA STANDARD; PRT; 5 AA.

AC P6164;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pardaxin II (PXII) (Fragment).  
OS Pardachirus marmoratus (Red sea moose sole).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleioidae; Soleidae; Pardachirus.  
OX NCBI\_TaxId=31087;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=3782138;  
RA Lazarovici P., Primor N., Loew L.M.;  
RT "Purification and pore-forming activity of two hydrophobic

RT polypeptides from the secretion of the Red sea moose sole (Pardachirus  
RT marmoratus).";  
RL J. Biol. Chem. 261:16704-16713(1986).  
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant  
CC properties. Forms voltage-dependent, ion-permeable channels in  
CC membranes. At high concentration causes cell membrane lysis.  
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the pardaxin family.  
CC -----  
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CC removed.  
CC -----  
CC Direct protein sequencing; Toxin.  
KW NON TER 5  
FT SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GF 10  
DB 1 GF 2

RESULT 22

PCT CARMA STANDARD; PRT; 5 AA.

AC P67857; P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 23-OCT-2004 (Rel. 45, Last annotation update)  
DE Procollin.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxId=6759;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=86232789; PubMed=2872661; DOI=10.1016/0196-9781(86)90063-X;  
RA Stangier J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of procollin in  
RT pericardial organs of the shore crab, Carcinus maenas.";  
RL Peptides 7:67-72(1986).  
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,  
CC modulates visceral and skeletal muscle in many arthropods.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Found in the crab pericardial organs.  
CC -----  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC Direct protein sequencing; Neuropeptide.  
KW SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YL 4  
DB 2 YL 3

RESULT 23



```

PRCT LIMPO
ID PRCT LIMPO STANDARD; PRT; 5 AA.
AC P67858; P01373; 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Procollin.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
NCBI_TaxID=6850;
[1]
RN
RP PROTEIN SEQUENCE.
MEDLINE=90287800; PubMed=2356151; DOI=10.1016/0196-9781(90)90072-D;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrove A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.
RT Identification of procollin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.;
RL Peptides 11:205-211(1990).
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Found in the crab pericardial organs.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A60411; A60411.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B460000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
Db 2 YL 3

RESULT 24
PRCT PERAM STANDARD; PRT; 5 AA.
ID PRCT PERAM STANDARD; PRT; 5 AA.
AC P67859; P01373; 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Procollin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
OC Blattidae; Blattellinae; Periplaneta.
NCBI_TaxID=6978;
[1]
RN
RP PROTEIN SEQUENCE.
MEDLINE=6074708; PubMed=576; DOI=10.1016/0024-3205(75)90134-4;
RA Starratt A.N., Brown B.E.;
RT Structure of the pentapeptide procollin, a proposed neurotransmitter
RT in insects.;
RL Life Sci. 17:1253-1256(1975).
[2]
RN
RP BIOLOGICAL SOURCE.
MEDLINE=8122865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (procollin) associated with an identified neuron.";
RL Science 213:567-569(1981).
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -1- TISSUE SPECIFICITY: Found in the lateral white neurons.
CC -----
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CC removed.
CC -----
DR PIR; A01644; HOROHA.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B460000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
Db 2 YL 3

RESULT 25
RBB32_LITRU STANDARD; PRT; 5 AA.
ID RBB32_LITRU STANDARD; PRT; 5 AA.
AC P62073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Rubellidin-3.2.
OS Rubella rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
OC Pelodytidae; Litoria.
NCBI_TaxID=104695;
[1]
RN
RP PROTEIN SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -----
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CC removed.
CC -----
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10
Db 2 GF 3

RESULT 26
TRAM3_ECOLI STANDARD; PRT; 5 AA.
ID TRAM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tram protein (Fragment).

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GN Name=tram;  
 OS Escherichia coli.  
 CC Plasmid IncFIR R100 (NR1).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 OK NCBI\_TaxId=562;  
 RN (1)  
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RP MEDLINE=88227859; PubMed=2836369;  
 RX Inamoto S., Yoshioaka Y., Ohtsubo E.;  
 RA "Identification and characterization of the products from the tram and  
 RT tram genes of plasmid R100.";  
 CC J. Bacteriol. 170:2749-2757(1988).  
 CC -1- FUNCTION: Transfer gene protein. Is involved in the conjugation  
 CC process of bacterial cells for the exchange of plasmid DNA.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the tram family.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; M20941; -; NOT ANNOTATED; CDS; Genomic DNA.  
 DR PIR; A32014; A32014.  
 DR Conjugation; DNA-binding; Plasmid.  
 KW NON TER  
 FT SEQUENCE 5 AA; 634 MW; 6B1B1AA43500000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EE 2  
 Db 4 EE 5

RESULT 27  
 ASP2\_LACSN STANDARD; PRT; 6 AA.  
 ID ASP2\_LACSN  
 AC P82655;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Acid shock protein 2 (Fragment).  
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
 CC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 CC Lactobacillus.  
 OK NCBI\_TaxId=1625;  
 RN (1)  
 RN PROTEIN SEQUENCE.  
 RP STRAIN=CBL;  
 RC MEDLINE=21322712; PubMed=1129463;  
 RA De Angelis M., Blini L., Pallini V., Cocconcelli P.S., Gobberti M.;  
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBL.";  
 RL Microbiology 147:1863-1873(2001).  
 CC -1- INDUCTION: Overexpressed in acid environments.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Direct protein sequencing.  
 KW NON TER  
 FT SEQUENCE 6 AA; 779 MW; 6AA45B5B132A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EX 3  
 Db 3 EX 4

RESULT 28  
 E101\_LITRU STANDARD; PRT; 6 AA.  
 ID E101\_LITRU  
 AC P82056;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Electricin-1.  
 OS Litoria rubella (Desert tree frog).  
 CC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Anura; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 OK NCBI\_TaxId=104895;  
 RN (1)  
 RN PROTEIN SEQUENCE.  
 RP TISSUE=Skin secretion;  
 RA Mahlitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Amidation; Amphibian defense peptide; Direct protein sequencing.  
 KW MOD RES  
 FT SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VP 6  
 Db 2 VP 3

RESULT 29  
 ASCL\_ALIAS STANDARD; PRT; 7 AA.  
 ID ASCL\_ALIAS  
 AC P84071;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Ascalin (Fragment).  
 OS Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 CC Allium.  
 OK NCBI\_TaxId=28911;  
 RN (1)  
 RN PROTEIN SEQUENCE, AND FUNCTION.  
 RP TISSUE=Bud;  
 RC PubMed=12126728; DOI=10.1016/S0196-9781(02)00032-3;  
 RX Wang H.X., Ng T.B.;  
 RA "Ascalin, a new anti-fungal peptide with human immunodeficiency virus  
 RT type 1 reverse transcriptase-inhibiting activity from shallot bulbs.";  
 RL Peptides 23:1025-1029(2002).  
 CC -1- FUNCTION: Has antifungal activity against B.ciherea. Inhibits HIV-  
 CC 1 reverse transcriptase.  
 CC -1- MISCELLANEOUS: Inhibits HIV-1 reverse transcriptase with an IC(50)

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CC      of 10 uM.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      Anticribobial; Direct protein sequencing; Fungicide.
CC      NON TER
CC      SEQUENCE 7 AA; 712 MW; 687866D87EA6CB30 CRC64;
SQ
Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 QG 9
DB      5 QG 6

RESULT 30
CAP6 CANAL STANDARD; PRT; 7 AA.
AC P83784;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DE Cytoplasmic antigenic protein 6 (Fragment).
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Microsporici Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND ANTIGENICITY.
RC STRAIN=SC5314; TISSUE=Protoplast;
PubMed=15378761; DOI=10.1002/pmic.200400903;
RA Pitarach A., Abian J., Carrascal M., Sanchez M., Nombela C., Gil C.;
RT "Proteomics-based identification of novel Candida albicans antigens
RT for diagnosis of systemic candidiasis in patients with underlying
RT hematological malignancies."
RL Proteomics 4:3084-3106(2004).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: Has antigenic properties. Elicits a specific immune
CC response in systemic candidiasis human patients undergoing
CC malignant hematological disorders.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Antigen; Direct protein sequencing.
CC NON TER
CC SEQUENCE 7 AA; 900 MW; 740736CD046DAC0 CRC64;
SQ
Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 QG 8
DB      4 QG 5

RESULT 31
CCP1_ENTPA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone CCP10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adair J.C., Dunn G.M., Suzuki A.;
RT "Structure of CCP10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCCP10."
RL J. Biol. Chem. 263:14574-14578(1988).
CC -1- FUNCTION: CCP10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCCP10.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A30812; A30812.
DR Direct protein sequencing; Pheromone.
KM SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
SQ
Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LV 5
DB      1 LV 2

RESULT 32
TPPY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Trypophyllin-1 (Pdt-1).
OS Pachymedusa daenicolior (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP PROTEIN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND
RP AMIDATION.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa daenicolior tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA."
RL Submitted (SEP-2002) to Swiss-Prot.
CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGS=1-7; NOTE=Ref.1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC GO; GO:0005576; C:extracellular region; NMS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NMS.
AMidation; Amphibian defense peptide; Direct protein sequencing;

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KW Hydroxylacton.
FT MOD RES 3 3 Hydroxyproline.
FT MOD RES 7 7 Proline amide.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 6 VP 7

RESULT 33
UP03 MOUSE STANDARD; PRT; 7 AA.
ID UP03_MOUSE
AC P38641;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P36) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Fibroblast;
RA MEDLINE=9500907; PubMed=7523108;
RX Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.,
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RU Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.1, its MW is: 36 kDa.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Direct protein sequencing.
CC
KW NON TER 7
FT SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B180 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2
DB 2 EE 3

RESULT 34
UH11 RAT STANDARD; PRT; 7 AA.
ID UH11_RAT
AC P56576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of heart tissue (Spot P11) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;

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RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.5, its MW is: 42 kDa.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Direct protein sequencing.
CC
KW UNSURE 2
FT NON TER 2
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9
DB 6 QG 7

RESULT 35
Q8NH7 HUMAN
ID Q8NH7_HUMAN PRELIMINARY; PRT; 7 AA.
AC Q8NH7
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Min-cistron.
GN Name=NEH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Malkooti J., Ramaswamy K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282824; AAMS3436.1; -; Genomic DNA.
SQ SEQUENCE 7 AA; 842 MW; 74072DC772D406F0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 3 VP 4

RESULT 36
Q28742 RABIT
ID Q28742_RABIT PRELIMINARY; PRT; 7 AA.
AC Q28742
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jokovic S.,

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RA Rabinowitz M.;  
RT "Characterization of genomic clones specifying rabbit alpha- and beta-  
RT ventricular myosin heavy chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048 (1984).  
DR EMBL; K01698; AAA31415.1; -; Genomic\_DNA.  
DR PIR; I46868; I46868.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EE 2  
DB 6 EE 7  
  
RESULT 37  
P93233\_LYCES PRELIMINARY; PRT; 7 AA.  
AC P93233;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)  
DE (Fragment).  
GN Name=L-ACSB;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
OX NCBI\_TaxID=4081;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97351561; PubMed=9207843; DOI=10.1023/A:1005800511372;  
RA Oelker J.H., Olson D.C., Shu O.Y., Yang S.F.;  
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate  
RT synthase genes by elicitor in suspension cultures of tomato  
RT (Lycopersicon esculentum).";  
RT Plant Mol. Biol. 34:275-286 (1997).  
DR EMBL; U75692; AAC49682.1; -; mRNA.  
DR GO; GO:0016647; P:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.  
DR CO; GO:0016629; P:lyase activity; IEA.  
KW Lyase.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LV 5  
DB 4 LV 5  
  
RESULT 38  
O9CSB3\_ARATH PRELIMINARY; PRT; 7 AA.  
ID O9CSB3\_ARATH  
AC O9CSB3;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein D1D1 10A-2b (Fragment).  
GN Name=D1D1 10A-2b;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Roots;  
RX MEDLINE=21171025; PubMed=11277426;  
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;  
RT "Arabidopsis thaliana genes expressed in the early compatible  
RT interaction with root-knot nematodes.";  
RL Mol. Plant Microbe Interact. 14:288-299 (2001).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Roots;  
RA Vercauteren I., J.R.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ286350; CAB71014.2; -; mRNA.  
KW Hypothetical protein.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LV 5  
DB 5 LV 6  
  
RESULT 39  
O8KMS9\_GENTR PRELIMINARY; PRT; 7 AA.  
ID O8KMS9\_GENTR  
AC O8KMS9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Putative transposase (Fragment).  
GN Name=tntA;  
OS Enterobacter sp. CH2-4.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=143777;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CH2-4;  
RX MEDLINE=21604134; PubMed=11763242; DOI=10.1016/S0923-2508(01)01265-7;  
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,  
RA Minakhin L.S., Kalyaeva B.S., Kopleva A.V., Petrova M.A.,  
RA Yuriev O.V., Nikiforov V.G.;  
RT "Mercury resistance transposons of gram-negative environmental  
RT bacteria and their classification.";  
RL Res. Microbiol. 152:811-822 (2001).  
DR EMBL; AJ302778; CAC83058.1; -; Genomic\_DNA.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DA9A0 CRC64;  
  
Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EE 2  
DB 5 EE 6  
  
RESULT 40  
O07354\_SYNP8 PRELIMINARY; PRT; 7 AA.  
ID O07354\_SYNP8  
AC O07354;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NifK (Fragment).  
GN Name=nifK;  
OS Synechococcus sp. (strain PCC 8801 / RP-1) (Cyanothace PCC 8801).  
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.

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OK NCBI_TaxID=41431;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.-C., Lin R.-F., Chu M.-K., Chen H.-M.,
RT "Organization and expression of nitrogen-fixation and aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RT RF-1."
RL Microbiology 145:743-753(1999).
DR EMBL; AF003700; AAC35193.1; -, Genomic_DNA.
FT NON TER
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5
DB 5 LV 6

RESULT 41
054248 STRGR PRELIMINARY; PRT; 7 AA.
ID 054248
AC 054248
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE RplO protein (Fragment).
GN Name=RplO;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeyer U.F.,
RT "Analysis and regulation of the secY gene from Streptomyces griseus
RT N2-3-11 and interaction of the secY protein with the SecA protein."
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CA65160.1; -, Genomic_DNA.
FT NON TER
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5
DB 6 LV 7

RESULT 42
08K3H6 RAT PRELIMINARY; PRT; 7 AA.
ID 08K3H6
AC 08K3H6
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Collagenase-3 (Fragment).
GN Name=Mmp13;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Earchontoglires; Glires; Rodentia; Sciurognath;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=Sprague-Dawley;
RA Prietco S.M., Lyons J.G.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101357; AAM51172.1; -, Genomic_DNA.
KW Collagen.
FT NON TER
FT NON TER
SQ SEQUENCE 7 AA; 907 MW; 63373B51B1BD9A0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
DB 5 YL 6

RESULT 43
09Y010 SCORO PRELIMINARY; PRT; 7 AA.
ID 09Y010
AC 09Y010
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7;
RA Raschecht D., Gelfi J., Laude H.;
RT "Enteric coronavirus TC8V: partial sequence of the genomic RNA, its
RT organization and expression."
RL Biochimie 69:591-600(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleuter J., Raschecht D., Lambert P., Levy L., Vende P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus."
RL Virology 206:817-822(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99099045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes."
RL J. Virol. 73:1535-1545(1999).
DR EMBL; AJ011482; CA09625.1; -, Genomic_RNA.
KW Hypothetical protein.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
DB 3 YL 4

RESULT 44
042564 FUGRU PRELIMINARY; PRT; 7 AA.
ID 042564
AC 042564
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).

```

GN Name=Scn8a;  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA PubMed=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;  
 RA Plummer N.W., McBurney M.W., Meisler M.H.;  
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated  
 RT two-domain protein in fetal brain and non-neuronal cells."  
 RL J. Biol. Chem. 272:24008-24015(1997).  
 DR EMBL; U93673; AAB80916.1; -, Genomic DNA.  
 DR GO; GO:0005216; P:ion channel activity; IEA.  
 KW Ionic channel.  
 KM NON TER  
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;  
 Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 5 VP 6  
 Db 1 VP 2  
 RESULT 45  
 ID OGBE81\_9HIV1 PRELIMINARY; PRT; 7 AA.  
 AC OGBE81;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Truncated pol protein (Fragment).  
 GN Name=pol;  
 OS Human immunodeficiency virus 1.  
 OS Viruses; Retroviral viruses; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 OC NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22056123; PubMed=12060770; DOI=10.1073/pnas.112177799;  
 RA Beerwinkkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,  
 RA Hoffmann D., Korn K., Selbig J.;  
 RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics  
 RT approach to predicting phenotype from genotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).  
 DR EMBL; AF347267; AAK32344.1; -, Genomic RNA.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;  
 Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 PQ 7  
 Db 1 PQ 2  
 RESULT 46  
 ID CAD1\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Sex pheromone CAD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI\_TaxID=1351;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872; DOI=10.1016/0014-5793(84)81248-X;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 RT induces plasmid transfer in Streptococcus faecalis."  
 RL FEBS Lett. 178:97-100(1984).  
 CC -1- FUNCTION: Involved in the conjugative transfer of the hemolysin  
 CC plasmid pAD1.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC Direct protein sequencing; Pheromone.  
 KM  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 LV 5  
 Db 4 LV 5  
 RESULT 47  
 ID CAP4\_CANAL STANDARD; PRT; 8 AA.  
 AC P83781;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Cytoplasmic antigenic protein 4 (Fragment).  
 GN Candida albicans (Yeast).  
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OC NCBI\_TaxID=5476;  
 RN [1]  
 RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND ANTIGENICITY.  
 RC STRAIN=SC5314; TISSUE=Protoplast;  
 RX PubMed=15378761; DOI=10.1002/pmic.200400903;  
 RA Pitarach A., Abian O., Carrascal M., Sanchez M., Nombela C., Gil C.,  
 RT "Proteomics-based identification of novel Candida albicans antigens  
 RT for diagnosis of systemic candidiasis in patients with underlying  
 RT hematological malignancies."  
 RL Proteomics 4:3084-3106(2004).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: Has antigenic properties. Elicits a specific immune  
 CC response in systemic candidiasis human patients undergoing  
 CC malignant hematological disorders.  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC Antigen; Direct protein sequencing.  
 KM  
 FT NON TER  
 SQ SEQUENCE 8 AA; 844 MW; 085772D2D5A1AA7 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 5 VP 6  
 Db 1 VP 2

Db 6 VP 7

## RESULT 48

CPD1\_ENTFA STANDARD; PRT; 8 AA.

AC P13269;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Sex pheromone CPD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCB1\_TaxID=1351;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=85040388; PubMed=6436978;

RA Suzuki A., Mori M., Sugakami Y., Isogai A., Fujino M., Kltada C.,

RA Craig R.A., Clewell D.B.;

RT "Isolation and structure of bacterial sex pheromone, CPD1.";

RL Science 226:849-850(1984).

CC -1- FUNCTION: CPD1 is involved in the conjugative transfer of the

bacteriocin plasmid pPDI.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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removed.

CC Direct protein sequencing; Pheromone.

KW SEQUENCE 8 AA; 913 MW; 865B729C682C729 CRC64;

SQ

Query Match 20.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LV 5

Db 2 LV 3

## RESULT 49

DYS4\_LIMSA

ID\_DYS4\_LIMSA STANDARD; PRT; 8 AA.

AC P82082;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Dynastin-4.

OS Limodynastes salmuni (Salmon-striped frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Limodynastinae; Limodynastes.

OX NCB1\_TaxID=39404;

RN [1]

RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion; Rattery M.J., Bowie J.H., Wallace J.C., Tyler M.V.;

RA Bradford A.M., Rattery M.J., Bowie J.H., Wallace J.C., Tyler M.V.;

RT "Peptides from Australian frogs. The structure of the dynastins from

RT Limodynastes salmuni and fletcherin from Limodynastes fletcheri.";

RL Aust. J. Chem. 46:1235-1244(1993).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- MASS SPECTROMETRY: MW=772; METHOD=FAE; RANGE=1-8; NOTE=Ref.1.

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removed.

CC Direct protein sequencing.

KW

SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LV 5

Db 2 LV 3

## RESULT 50

FUS5\_FUSO

ID\_FUS5\_FUSO STANDARD; PRT; 8 AA.

AC P81010;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Allergen Fus s 13596\* (Fragment).

OS Fusarium solani subsp. pisi (Nectria haematococca).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

OX NCB1\_TaxID=70791;

RN [1]

RP PROTEIN SEQUENCE.

RC STRAIN=IARI 3596; TISSUE=Mycelium;

RA Verma J., Gangal S.V.;

RT Submitted (JUL-1997) to Swiss-Prot.

CC -1- ALLERGEN: Causes an allergic reaction in human.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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removed.

CC Allergen; Direct protein sequencing.

KW FT NON TER

SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VP 6

Db 7 VP 8

Search completed: January 18, 2006, 21:05:50  
Job time : 165 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:57:58 ; Search time 39 Seconds  
(without alignments)  
24.671 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 10

Sequence: 1 EBYLVPOQGF 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

Database: PIR 80:\*

1: P1:\*

2: P12:\*

3: P13:\*

4: P14:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	7	2	S71299
2	3	30.0	9	2	PH0108
3	3	30.0	9	2	A41978
4	3	30.0	10	2	A61218
5	3	30.0	10	2	B61218
6	3	30.0	3	3	PQ0010
7	3	30.0	3	3	E37196
8	3	30.0	3	3	A23751
9	3	30.0	4	1	ECXNA
10	3	30.0	4	2	B43848
11	3	30.0	4	2	T46627
12	3	30.0	4	2	A25844
13	3	30.0	4	2	I54357
14	3	30.0	4	2	S55238
15	3	30.0	4	2	S09478
16	3	30.0	4	2	A32480
17	3	30.0	5	1	HOROMA
18	3	30.0	5	2	C41225
19	3	30.0	5	2	B37325
20	3	30.0	5	2	B22565
21	3	30.0	5	2	B61445
22	3	30.0	5	2	A61445
23	3	30.0	5	2	B61168
24	3	30.0	5	2	JH0253
25	3	30.0	5	2	A60521
26	3	30.0	5	2	A32014
27	3	30.0	5	2	A60411
28	3	30.0	6	2	S11556
29	3	30.0	6	2	A37765

30	2	20.0	6	2	B44510	hypothetical prote
31	2	20.0	6	2	I65546	MHC H2-L antigen -
32	2	20.0	6	2	PT0514	T-cell receptor be
33	2	20.0	6	2	A41946	T-cell receptor ga
34	2	20.0	7	2	A60224	Met-enkephalin-Arg
35	2	20.0	7	2	PQ0663	membrane protein -
36	2	20.0	7	2	A44428	platelet aggregati
37	2	20.0	7	2	PT0087	ribulose-bisphosph
38	2	20.0	7	2	B61491	seed protein ws-5
39	2	20.0	7	2	PQ0728	unidentified 5.0/1
40	2	20.0	7	2	S78024	ribosomal protein
41	2	20.0	7	2	H33098	180K exoantigen
42	2	20.0	7	2	PT0283	Ig heavy chain CRD
43	2	20.0	7	2	B39040	caldesmon, fas
44	2	20.0	7	2	PT0543	T-cell receptor be
45	2	20.0	7	2	PT0579	T-cell receptor be
46	2	20.0	7	2	PT0581	T-cell receptor be
47	2	20.0	7	2	PT0671	T-cell receptor be
48	2	20.0	7	2	PX0008	glucuronosyltransf
49	2	20.0	7	2	A38081	amine oxidase (cop
50	2	20.0	7	2	S45648	Na+-transporting A
51	2	20.0	7	2	PQ0777	NADH2 dehydrogenas
52	2	20.0	7	2	A38812	sex pheromone cCp1
53	2	20.0	7	2	I46868	alpha-myosin heavy
54	2	20.0	8	2	S16324	hypothetical prote
55	2	20.0	8	2	TI0952	hypothetical prote
56	2	20.0	8	2	B33099	158K exoantigen -
57	2	20.0	8	2	G33098	205K exoantigen -
58	2	20.0	8	2	PT0368	Ig gamma chain C r
59	2	20.0	8	2	PT0311	Ig heavy chain CRD
60	2	20.0	8	2	A38887	T-cell receptor ga
61	2	20.0	8	2	C39690	neural cell adhesi
62	2	20.0	8	2	S29272	locophenol-binding
63	2	20.0	8	2	B47594	aspartate kinase (
64	2	20.0	8	2	S45651	probable Na+-trans
65	2	20.0	8	2	A59495	Vesicle associated
66	2	20.0	8	2	PQ0726	unidentified 4.5/4
67	2	20.0	8	2	US0315	leucokinin V - Mad
68	2	20.0	8	2	I49404	prealbumin - weste
69	2	20.0	8	2	A42689	major postnaptic
70	2	20.0	8	2	A5180	neural proteinase
71	2	20.0	8	2	PC4373	telomeric and tetr
72	2	20.0	8	2	TI3818	cytochrome oxidase
73	2	20.0	8	2	S69165	ferredoxin a2 - Ja
74	2	20.0	8	2	S20162	leghemoglobin III
75	2	20.0	8	2	P60588	sperm-activating p
76	2	20.0	8	2	B60588	sperm-activating p
77	2	20.0	8	2	G60588	neuropeptide B - b
78	2	20.0	8	2	B24749	thymic factor - pi
79	2	20.0	9	1	YPRG	thymocyte growth p
80	2	20.0	9	2	A60957	litorin I - Austr
81	2	20.0	9	2	S07204	phyllotoxinlele
82	2	20.0	9	2	A61357	caldesmon - rabbit
83	2	20.0	9	2	A44873	caldesmon - rabbit
84	2	20.0	9	2	A61230	caldesmon beta ch
85	2	20.0	9	2	D24180	fibrinogen beta ch
86	2	20.0	9	2	C24180	translation elonga
87	2	20.0	9	2	D58503	endospem protein.
88	2	20.0	9	2	S70332	amine oxidase (cop
89	2	20.0	9	2	S70345	bradykinin - horn
90	2	20.0	9	2	S65433	Ig heavy chain CRD
91	2	20.0	9	2	PT0324	gastrin - domestic
92	2	20.0	9	2	C60070	T-cell receptor ga
93	2	20.0	9	2	G41946	peptidylglycine mo
94	2	20.0	9	2	A42266	T-cell receptor be
95	2	20.0	9	2	PH0942	locustamycinotropin I
96	2	20.0	9	2	A61620	venom protein HR-3
97	2	20.0	9	2	D44787	serum amyloid P-co
98	2	20.0	9	2	S10920	cytochrome-c oxida
99	2	20.0	9	2	B20569	60K Ca binding pro
100	2	20.0	9	2	S77984	enamelin I - bovin
101	2	20.0	9	2	PT0080	
102	2	20.0	9	2	S10784	

103	2	20.0	9	2	A28924	fructose-bisphosph
104	2	20.0	9	2	PC7074	translacton elonga
105	2	20.0	9	2	A43065	hydroxyproline-3-b
106	2	20.0	9	2	PD0027	pev-tachykinin - p
107	2	20.0	9	2	B60246	ornitho-kinin - ch
108	2	20.0	9	2	S15850	vitamin D3 26-mono
109	2	20.0	9	2	A26744	bradykinin-like pe
110	2	20.0	9	2	A61057	thr-6 bradykinin -
111	2	20.0	9	2	A60579	bradykinin-like pe
112	2	20.0	9	2	A61363	bradykinin - commo
113	2	20.0	9	2	A61358	bradykinin-like pe
114	2	20.0	10	1	XASNPC	angiotensin-conver
115	2	20.0	10	1	XAVI68	angiotensin-conver
116	2	20.0	10	1	ECLQIM	tachykinin I - mig
117	2	20.0	10	1	ECLQ3M	tachykinin III - m
118	2	20.0	10	1	ECLQ4M	tachykinin IV - mi
119	2	20.0	10	2	S65388	cytochrome-c oxida
120	2	20.0	10	2	A43405	6-phosphofructo-2-
121	2	20.0	10	2	S39392	calpain (EC 3.4.22
122	2	20.0	10	2	S33844	alpha-2-macroglobu
123	2	20.0	10	2	A46491	C3 homolog HX - in
124	2	20.0	10	2	A60410	beta-neoendorphin
125	2	20.0	10	2	A61337	caerulein - frog (
126	2	20.0	10	2	A13687	caerulein-like pep
127	2	20.0	10	2	B43590	pilin type A66 - A
128	2	20.0	10	2	S65728	hemoglobin, extrac
129	2	20.0	10	2	S70721	heat shock protein
130	2	20.0	10	2	JP0072	ribosomal protein
131	2	20.0	10	2	C38925	seed storage prote
132	2	20.0	10	2	PG0753	beta-fructofuranos
133	2	20.0	10	2	PS0209	24K protein 4407 -
134	2	20.0	10	2	A61622	vitellogenin, 190k
135	2	20.0	10	2	C39111	Ig heavy chain C r
136	2	20.0	10	2	PT0243	Ig heavy chain CRD
137	2	20.0	10	2	PT0284	Ig heavy chain CRD
138	2	20.0	10	2	PH1344	Ig heavy chain DJ
139	2	20.0	10	2	B45482	platelet activatin
140	2	20.0	10	2	S66214	cartilage oligomer
141	2	20.0	10	2	C39398	Fc mu (1gM) recept
142	2	20.0	10	2	E41946	small nuclear ribo
143	2	20.0	10	2	E41946	T-cell receptor ga
144	2	20.0	10	2	E41946	T-cell receptor ga
145	2	20.0	10	2	B18887	T-cell receptor ga
146	2	20.0	10	2	S65715	aryl hydrocarbon (
147	2	20.0	10	2	S65385	cytochrome-c oxida
148	2	20.0	10	2	S13224	vite protein - Agr
149	2	20.0	10	2	S06964	hypothetical prote
150	2	20.0	10	2	A43590	pilin type Ael - A
151	2	20.0	10	2	D28027	protein P7 - curle
152	2	20.0	10	2	PH0113	alpha-amylase (EC
153	2	20.0	10	2	S30348	clotting protein -
154	2	20.0	10	2	S43625	cytochrome-c oxida
155	2	20.0	10	2	S43630	cytochrome-c oxida
156	2	20.0	10	2	S43631	cytochrome-c oxida
157	2	20.0	10	2	B37196	bradykinin-potent
158	2	20.0	10	2	S66638	acetylcholinestera
159	2	20.0	10	2	F33932	Ig mu chain J regi
160	2	20.0	10	2	C54226	light-harvesting p
161	2	20.0	10	2	PG0785	NADH2 dehydrogenas
162	2	20.0	10	2	S74147	glyceraldehyde-3-P
163	2	20.0	10	2	H60787	sperm-activating p
164	2	20.0	10	2	G60787	sperm-activating p
165	2	20.0	10	2	G60787	sperm-activating p
166	2	20.0	10	2	G60787	sperm-activating p
167	2	20.0	10	2	G60787	sperm-activating p
168	2	20.0	10	2	G60787	sperm-activating p
169	2	20.0	10	2	G60787	sperm-activating p
170	2	20.0	10	2	B60588	sperm-activating p
171	2	20.0	10	2	G60588	sperm-activating p
172	2	20.0	10	2	G60588	sperm-activating p
173	2	20.0	10	2	D60527	sperm-activating p
174	2	20.0	10	2	C39572	sperm-activating p
175	2	20.0	10	2	C39572	sperm-activating p

176	2	20.0	10	2	F60527	sperm-activating p
177	2	20.0	10	2	G60527	sperm-activating p
178	2	20.0	10	2	G60527	sperm-activating p
179	2	20.0	10	2	G60527	sperm-activating p
180	2	20.0	10	2	E39572	sperm-activating p
181	2	20.0	10	2	D60788	sperm-activating p
182	2	20.0	10	2	E60788	sperm-activating p
183	2	20.0	10	2	G60788	sperm-activating p
184	2	20.0	10	2	F60589	sperm-activating p
185	2	20.0	10	2	G60589	sperm-activating p
186	2	20.0	10	2	D60589	sperm-activating p
187	2	20.0	10	2	F60588	sperm-activating p
188	2	20.0	10	2	B60589	sperm-activating p
189	2	20.0	10	2	A60527	sperm-activating p
190	2	20.0	10	2	A60787	sperm-activating p
191	2	20.0	10	2	A60588	sperm-activating p
192	2	20.0	10	2	A60788	sperm-activating p
193	2	20.0	10	2	PC2172	triacylglycerol 11
194	2	20.0	3	3	A42565	R-phycoerythrin al
195	1	10.0	3	3	A43391	TRH-like tripeptid
196	1	10.0	3	3	F37196	bradykinin-potent
197	1	10.0	3	3	PT0636	T-cell receptor be
198	1	10.0	3	3	PT0571	tyrosine protein k
199	1	10.0	3	3	178890	blood cell protein
200	1	10.0	3	3	S68328	

## ALIGNMENTS

## RESULT 1

ICL2 protein - Parametium tetraurelia (fragment)

C:Species: Parametium tetraurelia

C&gt;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

## C:Accession: S71299

R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Belsson, J.

Eur. J. Biochem. 238, 121-128, 1996

A&gt;Title: Characterization of centrin genes in Parametium.

A:Reference number: S71298; MUID:96248429; PMID:8665928

## A:Accession: S71299

A:Molecule type: protein

A:Residues: 1-7 &lt;MAD&gt;

A:Cross-references: UNIPARC:UP1000017B66B

A:Experimental source: strain d4-2

C:Genetics:

A:Genetic code: SGC5

Query Match 30.0%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
 DB 5 PQQ 7

## RESULT 2

## PH0108

late G1-69 protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

## C:Accession: PH0108

R:Nikaido, T.; Bradley, D.W.; Pardee, A.B.

Exp. Cell Res. 192, 102-109, 1991

A&gt;Title: Molecular cloning of transcripts that accumulate during the late G1 phase in cul

A:Reference number: PH0108; MUID:91078351; PMID:1984406

## A:Accession: PH0108

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-9 &lt;NIK&gt;

A:Cross-references: UNIPARC:UP1000017C6E9

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEY 3  
|||  
DB 7 EEY 9

## RESULT 3

A41978  
calliphorinamide 1 - bluebottle fly (Calliphora vomitoria)  
C/Species: Calliphora vomitoria  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Accession: A41978  
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A/Reference number: A41978; PMID:92196111; PMID:1549595  
A/Accession: A41978  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <DUV>  
A/Cross-references: UNIPROT:P41856; UNIPARC:UPI000012A50D  
C/Keywords: amidated carboxyl end; neuropeptide  
P/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
|||  
DB 2 PQQ 4

## RESULT 4

A61218  
alpha-glucan 4Ha - grass (Haynaldia villosa) (fragment)  
C/Species: Haynaldia villosa, Daespyrum villosum  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: A61218  
R/Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A/Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald  
A/Reference number: A61218; PMID:91315394; PMID:1859356  
A/Accession: A61218  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SHR>  
A/Cross-references: UNIPROT:Q7M1F7; UNIPARC:UPI000017CA45  
C/Keywords: seed; storage protein

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQ 7  
|||  
DB 6 VPQ 8

## RESULT 5

B61218  
alpha-glucan 6Ha - grass (Haynaldia villosa) (fragment)  
C/Species: Haynaldia villosa, Daespyrum villosum  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: B61218  
R/Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A/Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald  
A/Reference number: A61218; PMID:91315394; PMID:1859356  
A/Accession: B61218

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SHR>  
A/Cross-references: UNIPROT:Q7M1F6; UNIPARC:UPI000017B85  
C/Keywords: seed; storage protein

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPQ 7  
|||  
DB 5 VPQ 7

## RESULT 6

PQ0010  
angiotensin-converting enzyme inhibitor (FIP-3) - common fig  
N/Alternate names: ficus latex peptide 3  
C/Species: Ficus carica (common fig)  
C/Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C/Accession: PQ0010  
R/Maryama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A/Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A/Reference number: PQ0008  
A/Accession: PQ0010  
A/Molecule type: protein  
A/Residues: 1-3 <MAR>  
A/Cross-references: UNIPARC:UPI000011E971  
A/Experimental source: latex  
C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
|||  
DB 1 LV 2

## RESULT 7

E37196  
bradykinin-potentiating peptide 5 - island jararaca  
C/Species: Bothrops insularis (island jararaca)  
C/Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 30-Jun-2001  
C/Accession: E37196  
R/Cintre, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A/Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A/Reference number: A37196; PMID:90351557; PMID:2286615  
A/Accession: E37196  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-3 <GIN>  
A/Cross-references: UNIPARC:UPI0000158403  
C/Keywords: pyroglutamic acid  
P/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QQ 8  
|||  
DB 1 QQ 2

## RESULT 8

A23751  
spinal cord peptide SCP-4 - pig  
C/Species: Sus scrofa domestica (domestic pig)

C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
C/Accession: A23751  
R/Hs1, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.  
Arch. Biochem. Biophys. 240, 178-183, 1985  
A/Reference number: A23751; MUID:85250425; PMID:4015098  
A/Accession: A23751  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-3 <HS1>  
A/Cross-References: UNIPARC:UPI000017CE97

Query Match 20.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
||  
DB 1 QG 2

RESULT 9  
EXXAA  
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)  
C/Species: Anthopleura elegantissima  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A26666  
R/Grimmelikhuizen, C.J.P.; Graff, D.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
A/Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem  
A/Reference number: A26666; MUID:87092339; PMID:2879288  
A/Accession: A26666  
A/Molecule type: protein  
A/Residues: 1-4 <GRI>  
A/Cross-References: UNIPROT:P10419; UNIPARC:UPI00001733AF  
C/Comment: The function of this peptide is not known but it could act as a transmitter a  
C/Comment: Synthetic and natural peptides had identical properties.  
C/Superfamily: RFamide neuropeptide  
C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F.4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
||  
DB 1 QG 2

RESULT 10  
B43848  
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)  
C/Species: Staphylococcus aureus  
C/Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
C/Accession: B43848  
R/Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.  
Infect. Immun. 60, 899-906, 1992  
A/Title: Binding of heparan sulfate to Staphylococcus aureus.  
A/Reference number: A43848; MUID:92176005; PMID:1541563  
A/Accession: B43848  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-4 <LIA>  
A/Cross-References: UNIPARC:UPI000017ABF7  
A/Note: sequence extracted from NCBI backbone (NCBIP:85444)

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
||

DB 2 LV 3

RESULT 11  
T46627  
hypothetical protein c4 - loblolly pine  
C/Species: Pinus taeda (loblolly pine)  
C/Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
C/Accession: T46627  
R/Chang, S.; Puryear, J.; Funkhouser, B.A.; Newton, R.J.; Cairney, J.  
Submitted to the EMBL Data Library, July 1995  
A/Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do  
A/Reference number: Z23105  
A/Accession: T46627  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-4 <CHA>  
A/Cross-References: UNIPARC:UPI000011B913; EMBL:U31309; MUID:9974285; PID:9974292  
A/Experimental source: strain 66PTX66PT3; 8 month seedlings

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
||  
DB 3 LV 4

RESULT 12  
A25844  
antho-RF amide neuropeptide - sea pansy (Renilla koellikeri)  
C/Species: Renilla koellikeri (Koelliker's sea pansy)  
C/Date: 21-May-1998 #sequence\_revision 30-Sep-1993 #text\_change 11-Jul-1997  
C/Accession: A25844  
R/Grimmelikhuizen, C.J.P.; Groeger, A.  
PSS Lett. 211, 105-108, 1987  
A/Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renilla  
A/Reference number: A25844  
A/Accession: A25844  
A/Molecule type: protein  
A/Residues: 1-4 <GRI>  
A/Cross-References: UNIPARC:UPI00001733AF  
C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F.4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
||  
DB 1 QG 2

RESULT 13  
I54357  
schwannomin - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C/Accession: I54357  
R/Huynh, D.P.; Nechiporuk, T.; Pulst, S.  
Hum. Mol. Genet. 3, 1075-1079, 1994  
A/Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are cor  
A/Reference number: I54357; MUID:95072570; PMID:7981675  
A/Accession: I54357  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-4 <RSS>  
A/Cross-References: UNIPARC:UPI000011B801; GB:I28838; MUID:9454836; PIDN:AAA57150.1; PID:9  
A/Gene: NF2

Query Match 20.0%; Score 2; DB 2; Length 4;  
A:Note: stereochemistry of the active form confirmed by chemical synthesis  
Rishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto, FES Lett. 207, 253-256, 1992  
A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro (H-Gly-Phe-Ala-Asp-OH).  
A:Reference number: A44691; PMID:92354723; PMID:1644179  
A:Contents: annotation; X-ray crystallography, 0.85 angstroms  
A:Note: achatin-II has L-phenylalanine  
C:Keywords: D-amino acid  
F:2/Modified site: D-phenylalanine (Phe) #status experimental

RESULT 14  
555238  
pallidipin - asassasin bug (fragment)  
C:Species: Triatoma pallidipennis (asassasin bug)  
C>Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
C:Accession: S55238  
R:Haendler, B.; Becker, A.; Noeske-Dunplut, C.; Kraetzschmar, J.; Donner, P.; Schleunin Biochem. J. 307, 465-470, 1995  
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib A:Reference number: S55238; PMID:95251610; PMID:7733884  
A:Accession: S55238  
A:Molecule type: protein  
A:Residues: 1-4 <HAE>  
A:Cross-references: UNIPARC:UPI000017CB07

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2  
1 EE 2  
1 EE 2

Db 1 EE 2

RESULT 15  
S09478  
globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)  
N:Alternate names: 11S globulin alpha subunit gamma chain  
C:Species: Cucurbita sp. (cucurbit)  
C>Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 08-Nov-1996  
C:Accession: S09478  
R:Ohmura, M.; Hara, I.; Matsubara, H.  
Plant Cell Physiol. 21, 157-167, 1980  
A:Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A:Reference number: S09066  
A:Accession: S09478  
A:Molecule type: protein  
A:Residues: 1-4 <OHM>  
A:Cross-references: UNIPARC:UPI000017CB16

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 OG 9  
1 OG 9  
2 OG 3

Db 2 OG 3

RESULT 16  
A32480  
achatin-I - giant African snail  
N:Contains: achatin-II  
C:Species: Achatina fulica (giant African snail)  
C>Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 09-Jul-2004  
C:Accession: A32480  
R:Kametani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sut Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989  
A:Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru A:Reference number: A32480; PMID:9273551; PMID:2597281  
A:Accession: A32480  
A:Molecule type: protein  
A:Residues: 1-4 <KAM>

A:Cross-references: UNIPROT:P35904; UNIPARC:UPI0000125223  
A:Note: stereochemistry of the active form confirmed by chemical synthesis  
Rishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto, FES Lett. 207, 253-256, 1992  
A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro (H-Gly-Phe-Ala-Asp-OH).  
A:Reference number: A44691; PMID:92354723; PMID:1644179  
A:Contents: annotation; X-ray crystallography, 0.85 angstroms  
A:Note: achatin-II has L-phenylalanine  
C:Keywords: D-amino acid  
F:2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GP 10  
1 GP 2

Db 1 GP 2

RESULT 17  
H0R0H4  
proctolin - American cockroach  
C:Species: Periplaneta americana (American cockroach)  
C>Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 09-Jul-2004  
C:Accession: A01644  
R:Starratt, A.N.; Brown, B.E.  
Life Sci. 17, 1253-1256, 1975  
A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects. A:Reference number: A93048; PMID:76074708; PMID:576  
A:Accession: A01644  
A:Molecule type: protein  
A:Residues: 1-5 <STR>  
A:Cross-references: UNIPROT:P01373; UNIPARC:UPI0000132177  
A:Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac R:O'Shea, M.; Adams, M.E.  
Science 213, 567-569, 1981  
A:Title: Pentapeptide (proctolin) associated with an identified neuron.  
A:Reference number: A94260; PMID:81225865; PMID:6113690  
A:Contents: annotation; biological source  
C:Comment: This peptide is found in the lateral white neurons, which occur (in the cockr innervate the striated hindgut muscles in insects and stimulate contraction of these musc C:Superfamily: proctolin  
C:Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
1 YL 4  
2 YL 3

Db 2 YL 3

RESULT 18  
C41225  
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
C:Species: Pseudomonas syringae pv. tomato  
C>Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C:Accession: C41225  
R:Cha, J.S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer memt A:Reference number: A41225; PMID:92020961; PMID:1924351  
A:Accession: C41225  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <CHA>  
A:Cross-references: UNIPARC:UPI000017A984

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LV 5  
 DB 4 LV 5

## RESULT 19

B37325  
 pap fibribial regulatory protein pap1 - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C:Date: 11-Sep-1992 #sequence\_revision 11-Sep-1992 #text\_change 23-Mar-1993  
 C:Accession: B37325  
 R:Bratton, B.A.; Blym, L.B.; Skinner, B.S.; Low, D.A.  
 J:Biochem. 173, 1789-1800, 1991  
 A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap plus ex  
 A:Reference number: A37325; MUID:91154136; PMID:1671857  
 A:Accession: B37325  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <B3A>  
 A:Cross-references: UNIPARC:UPI000011B98D; GB:M63747

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 BY 3  
 DB 3 BY 4

## RESULT 20

B22565  
 R-phycoerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)  
 C:Species: Gastrocionium coulteri  
 C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
 C:Accession: B22565  
 R:Klotz, A.V.; Glazer, A.N.  
 J:Biol. Chem. 260, 4856-4863, 1985  
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A:Reference number: A22565; MUID:85182601; PMID:3886644  
 A:Accession: B22565  
 A:Molecule type: protein  
 A:Residues: 1-5 <KLO>  
 A:Cross-references: UNIPARC:UPI000017ABE3

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
 DB 3 VP 4

## RESULT 21

B61445  
 Leu-enkephalin - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C:Accession: B61445  
 R:Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A:Reference number: A61445; MUID:84144823; PMID:6583690  
 A:Accession: B61445  
 A:Molecule type: protein  
 A:Residues: 1-5 <LEU>  
 A:Cross-references: UNIPARC:UPI000002D557  
 A:Experimental source: pedal ganglia  
 C:Keywords: neuropeptide; opioid peptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 GF 10  
 DB 3 GF 4

## RESULT 22

A61445  
 Met-enkephalin - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C:Accession: A61445  
 R:Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A:Reference number: A61445; MUID:84144823; PMID:6583690  
 A:Accession: A61445  
 A:Molecule type: protein  
 A:Residues: 1-5 <LEU>  
 A:Cross-references: UNIPARC:UPI000002CF9B  
 A:Experimental source: pedal ganglia  
 C:Keywords: neuropeptide; opioid peptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
 DB 3 GF 4

## RESULT 23

B61168  
 cocoonase (BC 3.4.21.-) - Chinese oak silkworm (fragment)  
 C:Species: Antheraea pernyi (Chinese oak silkworm)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: B61168  
 R:Kramer, K.J.; Felsted, R.L.; Law, J.H.  
 J:Biol. Chem. 248, 3021-3028, 1973  
 A:Title: Cocoonase, V. Structural studies on an insect serine protease.  
 A:Reference number: A61168; MUID:73165540; PMID:4735570  
 A:Accession: B61168  
 A:Molecule type: protein  
 A:Residues: 1-5 <KRA>  
 A:Cross-references: UNIPARC:UPI000017BB47  
 A:Keywords: hydrolase; serine proteinase; zymogen  
 F:1-5/Product: cocoonase (fragment) #status experimental <MAT>

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
 DB 4 GF 5

## RESULT 24

JH0253  
 gut pentapeptide - Japanese eel  
 C:Species: Anguilla japonica (Japanese eel)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
 C:Accession: JH0253  
 R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
 Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
 A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
 A:Reference number: JH0253; MUID:92062113; PMID:1953755  
 A:Accession: JH0253  
 A:Molecule type: protein

A:Residues: 1-5 <UES>  
 A:Cross-references: UNIPARC:UPI000017BF42  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
 C:Accession: A60411  
 R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.  
 Peptides 11, 205-211, 1990  
 A:Title: Identification of proctolin in the central nervous system of the horseshoe crab,  
 and of the circular muscle of the gastro-intestinal junction.

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
 ||  
 DB 1 GF 2

RESULT 25  
 A60521  
 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N:Alternate names: glycogen phosphorylase b  
 C:Species: Liza ramada  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 15-Mar-2004  
 C:Accession: A60521  
 R:Bonamura, L.; Baanante, I.V.  
 Comp. Biochem. Physiol. B 95, 295-301, 1990  
 A:Title: Purification and characterization of glycogen phosphorylase B from skeletal mus  
 A:Reference number: A60521; PMID:90227907; PMID:2109669  
 A:Accession: A60521  
 A:Molecule type: protein  
 A:Residues: 1-5 <BON>  
 A:Cross-references: UNIPARC:UPI00001753C3  
 C:Keywords: glycocyltransferase; hexosyltransferase; phosphoprotein  
 P:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
 ||  
 DB 4 VP 5

## RESULT 26

A32014  
 traw protein - Escherichia coli plasmid R100 (fragment)

C:Species: Escherichia coli  
 C:Date: 22-Jun-1989 #sequence\_revision 22-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: A32014  
 R:Imamoto, S.; Yoshioke, Y.; Ohtsubo, E.  
 J. Bacteriol. 170, 2749-2757, 1988  
 A:Title: Identification and characterization of the products from the traw and traw gene  
 A:Reference number: A32014; PMID:88227859; PMID:2836369  
 A:Accession: A32014  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <INA>  
 A:Cross-references: UNIPROT:P13973; UNIPARC:UPI000011ECA2  
 C:Genetics:  
 A:Genome: plasmid  
 C:Keywords: DNA binding

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EB 2  
 ||  
 DB 4 EB 5

## RESULT 27

A60411  
 proctolin - Atlantic horseshoe crab

C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
 C:Accession: A60411  
 R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.  
 Peptides 11, 205-211, 1990  
 A:Title: Identification of proctolin in the central nervous system of the horseshoe crab,  
 and of the circular muscle of the gastro-intestinal junction.  
 A:Reference number: A60411; PMID:90287800; PMID:2356151  
 A:Accession: A60411  
 A:Molecule type: protein  
 A:Residues: 1-5 <GRO>  
 A:Cross-references: UNIPROT:P01373; UNIPARC:UPI0000132177  
 C:Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse  
 C:Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
 ||  
 DB 2 YL 3

## RESULT 28

S11556  
 hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)

N:Alternate names: bisulfite reductase; desulfofuscidin  
 C:Species: Desulfovibrio thermophilus  
 C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
 C:Accession: S11556  
 R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; Le  
 Bichlm. Biophys. Acta 1040, 112-118, 1990  
 A:Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from  
 A:Reference number: S11024; PMID:90335276; PMID:2165817  
 A:Accession: S11556  
 A:Molecule type: protein  
 A:Residues: 1-6 <FAU>  
 A:Cross-references: UNIPARC:UPI000017AB75  
 C:Keywords: oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EB 2  
 ||  
 DB 2 EB 3

## RESULT 29

A37765  
 hypothetical protein (csmA 5' region) - Chloroflexus aurantiacus (fragment)

C:Species: Chloroflexus aurantiacus  
 C:Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
 C:Accession: A37765  
 R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
 J. Bacteriol. 172, 4497-4504, 1990  
 A:Title: Gene encoding the 5'-kilodalton chlorosome protein of Chloroflexus aurantiacus:  
 A:Reference number: A37765; PMID:9030558; PMID:2376566  
 A:Accession: A37765  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-6 <THE>  
 A:Cross-references: UNIPARC:UPI000017ABA1; GB:M33964

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQ 7  
 ||  
 DB 1 PQ 2

```

RESULT 30
B44510
Hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)
C:Species: Lactococcus lactis
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C:Accession: B44510
R:Renault, P.; Galliardin, C.; Heslot, H.
J. Bacteriol. 171, 3108-3114, 1989
A:Title: Product of the Lactococcus lactis gene required for malolactic fermentation is
A:Reference number: A44510; MUID:89255069; PMID:2498286
A:Accession: B44510
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-6 <REN>
A:Cross-references: UNIPARC:UPI000017AC46; EMBL:M90762

Query Match
20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3 YL 4
||
Db 5 YL 6

RESULT 31
I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RSS>
A:Cross-references: UNIPARC:UPI000011B8A9; GB:M12483; NID:G199565; PIDN:AAA39663.1; PID:

Query Match
20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5 VP 6
||
Db 2 VP 3

RESULT 32
PT0514
T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0514
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0514
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEF>
A:Cross-references: UNIPARC:UPI000017C7B4
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match
20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      8  Q3  9
      ||
DB      5  Q3  6

RESULT 33
A41946
T-cell receptor gamma chain (1c.22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma germline DNA
A:Reference number: A41946; MUID:92049316; PMID:1558619
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 16 <MHE>
A:Cross-references: UNIPARC:UPI000017C865
C:Keywords: T-cell receptor

Query Match      20.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9  GF 10
      ||
DB      5  GF 6

RESULT 34
A60224
Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Bech, F.S.; Boehlen, P.; Makle, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A:Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91225680; PMID:2027006
A:Accession: A60224
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Cross-references: UNIPARC:UPI00000352EB
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opioid peptide

Query Match      20.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9  GF 10
      ||
DB      3  GF 4

RESULT 35
P00663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: P00663
R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
isoleucine gastroenteritis virus.
A:Reference number: JQ2191; MUID:93389433; PMID:8397280
A:Accession: P00663
A:Molecule type: mRNA
A:Residues: 1-7 <BRI>
A:Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:6

```



C/Comment: This virus is coronavirus related to human coronavirus 229E.  
C/Keywords: membrane protein

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
DB 6 LV 7

## RESULT 36

A44428  
platelet aggregation-associated protein - Streptococcus sanguis (fragment)  
C/Species: Streptococcus sanguis  
C/Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 11-Nov-1994  
C/Accession: A44428  
R/Brickson, P.R.; Herzberg, M.C.  
J. Biol. Chem. 268, 1646-1649, 1993  
A/Title: The Streptococcus sanguis platelet aggregation-associated protein. Identification  
A/Reference number: A44428; MUID:93131902; PMID:8420939  
A/Accession: A44428  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <ERI>  
A/Cross-references: UNIPARC:UPI000017AC2A  
C/Keywords: cell wall

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QG 9  
DB 4 QG 5

## RESULT 37

PT0087  
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (frag  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 24-Nov-1999  
C/Accession: PT0087  
R/Yagita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JEPD, December 1995  
A/Description: Two dimensional electrophoresis of plant proteins and standardization of  
A/Reference number: PN0173  
A/Accession: PT0087  
A/Molecule type: protein  
A/Residues: 1-7 <TSU>  
A/Cross-references: UNIPARC:UPI000017B001  
A/Experimental source: leaf  
C/Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase  
P.1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQ 7  
DB 2 PQ 3

## RESULT 38

B61491  
seed protein w8-5 - winged bean (fragment)  
C/Species: Psophocarpus tetragonolobus (winged bean)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C/Accession: B61491  
R/Hirano, H.  
J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dim

A/Reference number: A61491; MUID:89351606; PMID:2765119  
A/Accession: B61491  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <HIR>  
A/Cross-references: UNIPARC:UPI000017B074  
C/Keywords: glycoprotein; seed

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 3 VP 4

## RESULT 39

PQ0728  
unidentified 5.0/16k protein [imported] - rice (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C/Accession: PQ0728  
R/Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
A/Reference number: PQ0696  
A/Accession: PQ0728  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <KOM>  
A/Cross-references: UNIPARC:UPI000017B123

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
DB 5 LV 6

## RESULT 40

S78024  
ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)  
C/Species: Saccharomyces cerevisiae  
C/Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997  
C/Accession: S78024  
R/Kitakawa, M.; Graack, H.R.; Grobmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmar  
Bur. J. Biochem. 245, 449-456, 1997  
A/Title: Identification and characterization of the genes for mitochondrial ribosomal pr  
A/Reference number: S78018; MUID:97296414; PMID:9151978  
A/Accession: S78024  
A/Molecule type: protein  
A/Residues: 1-7 <KIT>  
A/Cross-references: UNIPARC:UPI000017B33C  
C/Genetics: nuclear  
A/Genome: nuclear  
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4  
DB 1 YL 2

## RESULT 41

H33098  
180K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum  
 C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: H33098  
 R:Nichols, J.H.; Hager, L.P.  
 Submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: H33098  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <NIC>  
 A:Cross-references: UNIPARC:UPI000017B5E2

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GF 10  
 DB 2 GF 3

## RESULT 42

PT0283  
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0283  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caeon, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0283  
 A:Molecule type: DNA  
 A:Residues: 1-7 <YAM>  
 A:Cross-references: UNIPARC:UPI000017C206  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QQ 8  
 DB 4 QQ 5

## RESULT 43

B39040  
 calsequestrin, fast skeletal muscle - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 23-Feb-1997  
 C:Accession: B39040  
 R:Gale, S.E.; Jones, L.R.  
 J. Biol. Chem. 266, 391-398, 1991  
 A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein  
 A:Reference number: A39040; MUID:91093153; PMID:1985907  
 A:Accession: B39040  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <CAL>  
 A:Cross-references: UNIPARC:UPI000017C5B8  
 C:Keywords: phosphoprotein; skeletal muscle

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EE 2  
 DB 3 EE 4

## RESULT 44

PT0543  
 T-cell receptor beta chain V-D-J region (126-18B) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0543  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0543  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FEE>  
 A:Cross-references: UNIPARC:UPI000017C80B  
 A:Experimental source: day 18 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QQ 9  
 DB 6 QQ 7

## RESULT 45

PT0579  
 T-cell receptor beta chain V-D-J region (141-1N) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0579  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0579  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FEE>  
 A:Cross-references: UNIPARC:UPI000017C83B  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QQ 9  
 DB 6 QQ 7

## RESULT 46

PT0581  
 T-cell receptor beta chain V-D-J region (159-1A) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0581  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0581  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FEE>  
 A:Cross-references: UNIPARC:UPI000017C83B  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 OG 9  
Db 6 OG 7

## RESULT 47

T-cell receptor beta chain V-D-J region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 04-Mar-2000

C/Accession: PT0671; PT0564; PT0537; PT0536; PT0682

R/Feeney, A.J. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A/Reference number: PT0509; MUID:91277601; PMID:1711558

A/Accession: PT0671

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-7 <FER>

A/Cross-references: UNIPARC:UPI000017C84A

A/Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1K

A/Accession: PT0564

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-6 <FRI>

A/Cross-references: UNIPARC:UPI000017C84B

A/Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1CE

A/Accession: PT0537

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-6 <FE2>

A/Cross-references: UNIPARC:UPI000017C84B

A/Experimental source: adult thymus, strain BALB/c, clone 126-1CH

A/Accession: PT0536

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-3 <FE3>

A/Cross-references: UNIPARC:UPI000017C84C

A/Experimental source: adult thymus, strain BALB/c, clone 126-1CC

A/Accession: PT0682

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-3 <FE4>

A/Cross-references: UNIPARC:UPI000017C84C

A/Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1B

C/Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 OG 9  
Db 5 OG 6

## RESULT 48

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N/Alternate names: UDP-glucuronosyltransferase

C/Species: Rattus norvegicus (Norway rat)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997

C/Accession: PX0008

R/Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A/Title: Purification and properties of a form of UDP-glucuronosyltransferase from liver

A/Reference number: PX0008; MUID:9197852; PMID:3149280

A/Accession: PX0008

A/Molecule type: protein

A/Residues: 1-7 <YOK>

A/Cross-references: UNIPARC:UPI000017C913  
C/Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LV 5  
Db 4 LV 5

## RESULT 49

amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (Pichia angusta) (fragment)

A/Accession: A38081

C/Species: Pichia angusta

C/Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 20-Apr-2000

C/Accession: A38081

R/Mu, D.; Jones, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Kliman, J.P.

J. Biol. Chem. 267, 7979-7982, 1992

A/Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine

A/Reference number: A38081; MUID:92235001; PMID:1569055

A/Accession: A38081

A/Molecule type: protein

A/Residues: 1-7 <MDA>

A/Cross-references: UNIPARC:UPI000017CA48

C/Keywords: copper; oxidoreductase; quinoprotein; topaquinone

P/4/Modified site: topaquinone (Tyr) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EV 3  
Db 5 EV 6

## RESULT 50

Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - Acetobacterium woodii (fragment)

N/Alternate names: ATPase alpha chain

C/Species: Acetobacterium woodii

C/Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999

C/Accession: S45648

R/Reidinger, J.; Mueller, V.

Eur. J. Biochem. 223, 275-283, 1994

A/Title: Purification of ATP synthase from Acetobacterium woodii and identification as a

A/Reference number: S45648; MUID:94307271; PMID:8033902

A/Accession: S45648

A/Molecule type: protein

A/Residues: 1-34-7 <REI>

A/Cross-references: UNIPARC:UPI000017CA11; UNIPARC:UPI000017CA12

A/Experimental source: DSM 1030

C/Keywords: hydrolase

Query Match 20.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EV 2  
Db 5 EV 6

Search completed: January 18, 2006, 21:06:35  
Job time : 42 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:49:16 : Search time 112 Seconds  
(without alignments)  
876.695 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EESRRARDPQRVYQINBDL.....AVENPEYLPGGAAPQHP 235

Scoring table:

OLIGO

Searched: 1867569 seqs, 417829326 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1241939

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database:

Published Applications AA Main: \*  
1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep: \*  
2: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep: \*  
3: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep: \*  
4: /cgn2\_6/prodata/1/pubppa/US10A\_PUBCOMB.pep: \*  
5: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep: \*  
6: /cgn2\_6/prodata/1/pubppa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	75.7	224	5	US-10-149-138-3713
2	132	56.2	217	3	US-09-821-883-25
3	132	56.2	217	6	US-11-144-912-25
4	84	35.7	86	4	US-10-029-186-29225
5	59	25.1	59	3	US-09-854-356-5
6	45	19.1	79	4	US-10-425-115-217661
7	39	16.6	135	3	US-09-925-301-1232
8	37	15.7	221	5	US-10-484-067-7
9	15	6.4	15	3	US-09-354-533-51
10	15	6.4	15	3	US-09-354-533-52
11	15	6.4	15	3	US-09-354-533-53
12	15	6.4	15	3	US-09-354-533-54
13	15	6.4	15	3	US-09-354-533-55
14	15	6.4	15	4	US-10-245-871-581
15	15	6.4	15	4	US-10-149-138-3722
16	15	6.4	15	4	US-10-149-138-3738
17	15	6.4	15	4	US-10-149-138-3739
18	15	6.4	15	4	US-10-149-138-3740
19	15	6.4	15	4	US-10-149-138-3743
20	15	6.4	15	4	US-10-149-138-3748
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22	15	6.4	15	4	US-10-149-138-3756
23	15	6.4	15	4	US-10-149-138-3769
24	15	6.4	15	4	US-10-149-138-3793
25	15	6.4	15	4	US-10-149-138-3812
26	15	6.4	15	4	US-10-149-138-3813
27	15	6.4	15	4	US-10-149-138-3832

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31	15	6.4	15	4	US-10-149-138-3858	Sequence 3858, Ap
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33	15	6.4	15	4	US-10-149-138-3870	Sequence 3870, Ap
34	15	6.4	15	4	US-10-149-138-3882	Sequence 3882, Ap
35	15	6.4	15	4	US-10-149-138-3911	Sequence 3911, Ap
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37	15	6.4	15	4	US-10-149-138-3917	Sequence 3917, Ap
38	15	6.4	15	4	US-10-149-138-3918	Sequence 3918, Ap
39	15	6.4	15	4	US-10-149-138-3923	Sequence 3923, Ap
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60	15	6.4	15	4	US-10-253-286-581	Sequence 581, Ap
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63	15	6.4	15	4	US-10-647-005-583	Sequence 53, Ap
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65	15	6.4	15	4	US-10-647-005-585	Sequence 55, Ap
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95	15	6.4	15	4	US-10-149-138-3944	Sequence 3944, Ap
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97	15	6.4	15	4	US-10-149-138-4487	Sequence 4487, Ap
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102	15	6.4	15	4	US-10-149-138-4543	Sequence 4543, Ap	175	11	4.7	11	4	US-10-149-138-1598	Sequence 1598, Ap
103	15	6.4	15	4	US-10-149-138-4544	Sequence 4544, Ap	176	11	4.7	11	4	US-10-149-138-1689	Sequence 1689, Ap
104	15	6.4	15	4	US-10-149-138-4545	Sequence 4545, Ap	177	11	4.7	11	4	US-10-149-138-1692	Sequence 1692, Ap
105	15	6.4	15	4	US-10-149-138-4546	Sequence 4546, Ap	178	11	4.7	11	4	US-10-149-138-1798	Sequence 1798, Ap
106	15	6.4	15	4	US-10-149-138-4547	Sequence 4547, Ap	179	11	4.7	11	4	US-10-149-138-1805	Sequence 1805, Ap
107	15	6.4	15	4	US-10-149-138-4548	Sequence 4548, Ap	180	11	4.7	11	4	US-10-149-138-1817	Sequence 1817, Ap
108	15	6.4	15	4	US-10-149-138-4549	Sequence 4549, Ap	181	11	4.7	11	4	US-10-149-138-1858	Sequence 1858, Ap
109	15	6.4	15	4	US-10-149-138-4550	Sequence 4550, Ap	182	11	4.7	11	4	US-10-149-138-1866	Sequence 1866, Ap
110	15	6.4	15	4	US-10-149-138-4551	Sequence 4551, Ap	183	11	4.7	11	4	US-10-149-138-1896	Sequence 1896, Ap
111	15	6.4	15	6	US-11-121-347-51	Sequence 51, Appl	184	11	4.7	11	4	US-10-149-138-1928	Sequence 1928, Ap
112	15	6.4	15	6	US-11-121-347-52	Sequence 52, Appl	185	11	4.7	11	4	US-10-149-138-1938	Sequence 1938, Ap
113	15	6.4	15	6	US-11-121-347-53	Sequence 53, Appl	186	11	4.7	11	4	US-10-149-138-1945	Sequence 1945, Ap
114	15	6.4	15	6	US-11-121-347-54	Sequence 54, Appl	187	11	4.7	11	4	US-10-149-138-1952	Sequence 1952, Ap
115	15	6.4	15	6	US-11-121-347-55	Sequence 55, Appl	188	11	4.7	11	4	US-10-149-138-1963	Sequence 1963, Ap
116	13	5.5	13	4	US-10-001-546-45	Sequence 45, Appl	189	11	4.7	11	4	US-10-149-138-1970	Sequence 1970, Ap
117	13	5.5	13	5	US-10-948-707-1219	Sequence 1219, Ap	190	11	4.7	11	4	US-10-149-138-2014	Sequence 2014, Ap
118	12	5.1	12	4	US-10-245-871-574	Sequence 574, Ap	191	11	4.7	11	4	US-10-149-138-2017	Sequence 2017, Ap
119	12	5.1	12	4	US-10-253-286-574	Sequence 574, Ap	192	11	4.7	11	4	US-10-149-138-2026	Sequence 2026, Ap
120	11	4.7	11	3	US-09-017-743C-118	Sequence 118, Ap	193	11	4.7	11	4	US-10-149-138-2047	Sequence 2047, Ap
121	11	4.7	11	3	US-09-017-743C-119	Sequence 119, Ap	194	11	4.7	11	4	US-10-149-138-2097	Sequence 2097, Ap
122	11	4.7	11	4	US-10-149-138-108	Sequence 108, Ap	195	11	4.7	11	4	US-10-149-138-2154	Sequence 2154, Ap
123	11	4.7	11	4	US-10-149-138-120	Sequence 120, Ap	196	11	4.7	11	4	US-10-149-138-2226	Sequence 2226, Ap
124	11	4.7	11	4	US-10-149-138-123	Sequence 123, Ap	197	11	4.7	11	4	US-10-149-138-2228	Sequence 2228, Ap
125	11	4.7	11	4	US-10-149-138-125	Sequence 125, Ap	198	11	4.7	11	4	US-10-149-138-2244	Sequence 2244, Ap
126	11	4.7	11	4	US-10-149-138-212	Sequence 212, Ap	199	11	4.7	11	4	US-10-149-138-2281	Sequence 2281, Ap
127	11	4.7	11	4	US-10-149-138-230	Sequence 230, Ap	200	11	4.7	11	4	US-10-149-138-2281	Sequence 2281, Ap
128	11	4.7	11	4	US-10-149-138-292	Sequence 292, Ap							
129	11	4.7	11	4	US-10-149-138-299	Sequence 299, Ap							
130	11	4.7	11	4	US-10-149-138-342	Sequence 342, Ap							
131	11	4.7	11	4	US-10-149-138-419	Sequence 419, Ap							
132	11	4.7	11	4	US-10-149-138-438	Sequence 438, Ap							
133	11	4.7	11	4	US-10-149-138-451	Sequence 451, Ap							
134	11	4.7	11	4	US-10-149-138-523	Sequence 523, Ap							
135	11	4.7	11	4	US-10-149-138-529	Sequence 529, Ap							
136	11	4.7	11	4	US-10-149-138-560	Sequence 560, Ap							
137	11	4.7	11	4	US-10-149-138-582	Sequence 582, Ap							
138	11	4.7	11	4	US-10-149-138-590	Sequence 590, Ap							
139	11	4.7	11	4	US-10-149-138-592	Sequence 592, Ap							
140	11	4.7	11	4	US-10-149-138-597	Sequence 597, Ap							
141	11	4.7	11	4	US-10-149-138-606	Sequence 606, Ap							
142	11	4.7	11	4	US-10-149-138-610	Sequence 610, Ap							
143	11	4.7	11	4	US-10-149-138-611	Sequence 611, Ap							
144	11	4.7	11	4	US-10-149-138-681	Sequence 681, Ap							
145	11	4.7	11	4	US-10-149-138-702	Sequence 702, Ap							
146	11	4.7	11	4	US-10-149-138-728	Sequence 728, Ap							
147	11	4.7	11	4	US-10-149-138-746	Sequence 746, Ap							
148	11	4.7	11	4	US-10-149-138-805	Sequence 805, Ap							
149	11	4.7	11	4	US-10-149-138-806	Sequence 806, Ap							
150	11	4.7	11	4	US-10-149-138-845	Sequence 845, Ap							
151	11	4.7	11	4	US-10-149-138-888	Sequence 888, Ap							
152	11	4.7	11	4	US-10-149-138-899	Sequence 899, Ap							
153	11	4.7	11	4	US-10-149-138-968	Sequence 968, Ap							
154	11	4.7	11	4	US-10-149-138-1005	Sequence 1005, Ap							
155	11	4.7	11	4	US-10-149-138-1032	Sequence 1032, Ap							
156	11	4.7	11	4	US-10-149-138-1039	Sequence 1039, Ap							
157	11	4.7	11	4	US-10-149-138-1147	Sequence 1147, Ap							
158	11	4.7	11	4	US-10-149-138-1161	Sequence 1161, Ap							
159	11	4.7	11	4	US-10-149-138-1280	Sequence 1280, Ap							
160	11	4.7	11	4	US-10-149-138-1290	Sequence 1290, Ap							
161	11	4.7	11	4	US-10-149-138-1470	Sequence 1470, Ap							
162	11	4.7	11	4	US-10-149-138-1486	Sequence 1486, Ap							
163	11	4.7	11	4	US-10-149-138-1495	Sequence 1495, Ap							
164	11	4.7	11	4	US-10-149-138-1513	Sequence 1513, Ap							
165	11	4.7	11	4	US-10-149-138-1538	Sequence 1538, Ap							
166	11	4.7	11	4	US-10-149-138-1553	Sequence 1553, Ap							
167	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							
168	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							
169	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							
170	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							
171	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							
172	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							
173	11	4.7	11	4	US-10-149-138-1576	Sequence 1576, Ap							

## ALIGNMENTS

RESULT 1  
US-10-484-067-13Sequence 13, Application US/10484067  
Publication No. US20040241686A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF CALIFORNIA

TITLE OF INVENTION: HBR2/NEU TARGET ANTIGEN AND USE OF SAME TO STIMULATE AN IMMUNE RES

FILE REFERENCE: UC11170-1

CURRENT FILING DATE: 2004-01-15

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: US 60/306,250

SOFTWARE: Patentin version 3.1

SEQU ID NO 13

LENGTH: 224

TYPE: PRT

ORGANISM: Homo sapiens

US-10-484-067-13

Query Match 75.7% Score 178 DB 5 Length 224

Best Local Similarity 100.0% Pred. No. 7.5e-149

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 58 CDDPAPGAGMWHRRSSSTRSGGDTLGLFPEBEERAPRPLAPSGAGSDVDDG 117
    |||
DB 1 CDDPAPGAGMWHRRSSSTRSGGDTLGLFPEBEERAPRPLAPSGAGSDVDDG 60
    |||
QY 118 MGAAGLGLSLPHDPSPLORYSSEDTVPLEPSSTDVVAPLTCSPOPEYVNOQDVAPQPS 177
    |||
DB 61 MGAAGLGLSLPHDPSPLORYSSEDTVPLEPSSTDVVAPLTCSPOPEYVNOQDVAPQPS 120
    |||
QY 178 PREGPLPARPAGATLERPKTLSPGKNGVVDVAFGGAIVENPEYLTTPGGAAPQHP 235
    |||
DB 121 PREGPLPARPAGATLERPKTLSPGKNGVVDVAFGGAIVENPEYLTTPGGAAPQHP 178
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```

RESULT 2

US-09-821-883-25  
Sequence 25, Application US/09821883  
Patent No. US20020061310A1  
GENERAL INFORMATION:  
APPLICANT: Laus, Reiner  
APPLICANT: Vidovic, Damir  
APPLICANT: Gradalis, Thomas  
TITLE OF INVENTION: Compositions and Methods for Dendritic  
FILE REFERENCE: 7636-0022.30  
CURRENT APPLICATION NUMBER: US/09/821,883  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: US 60/193,504  
PRIOR FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 217  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-821-883-25

Query Match 56.2%; Score 132; DB 3; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGGVMHRRHSSTSGGDLTLGLPSEBEPSPPLAPSEAGSDVDFDGLGMAAG 123  
DB 1 GAGGVMHRRHSSTSGGDLTLGLPSEBEPSPPLAPSEAGSDVDFDGLGMAAG 60

QY 124 LQSLPTHDSPLQRYSDPTVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 183  
DB 61 LQSLPTHDSPLQRYSDPTVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 120

QY 184 PAARPAGATLER 195  
DB 121 PAARPAGATLER 132

RESULT 3  
US-11-144-912-25  
Sequence 25, Application US/11144912  
Publication No. US20050232932A1  
GENERAL INFORMATION:  
APPLICANT: Laus, Reiner  
APPLICANT: Vidovic, Damir  
APPLICANT: Gradalis, Thomas  
TITLE OF INVENTION: Compositions and Methods for Dendritic  
FILE REFERENCE: 7636-0022.30  
CURRENT APPLICATION NUMBER: US/11/144,912  
CURRENT FILING DATE: 2005-06-03  
PRIOR APPLICATION NUMBER: US/09/821,883  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: US 60/193,504  
PRIOR FILING DATE: 2000-03-30  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 217  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-11-144-912-25

Query Match 56.2%; Score 132; DB 6; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GAGGVMHRRHSSTSGGDLTLGLPSEBEPSPPLAPSEAGSDVDFDGLGMAAG 123  
DB 1 GAGGVMHRRHSSTSGGDLTLGLPSEBEPSPPLAPSEAGSDVDFDGLGMAAG 60

QY 124 LQSLPTHDSPLQRYSDPTVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 183  
DB 61 LQSLPTHDSPLQRYSDPTVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 120

QY 184 PAARPAGATLER 195  
DB 121 PAARPAGATLER 132

DB 61 LQSLPTHDSPLQRYSDPTVPLPSETDGYVAPLTCSPQPEYVNOQDVAPQPPSPREGPL 120  
QY 184 PAARPAGATLER 195  
DB 121 PAARPAGATLER 132

RESULT 4  
US-10-029-386-29225  
Sequence 29225, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
FILE REFERENCE: AEMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 29225  
LENGTH: 88  
TYPE: PRF  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR17.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.91  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6  
OTHER INFORMATION: SWISSPROT HIT: P04626, EVALU6 6.00e-45  
US-10-029-386-29225

Query Match 35.7%; Score 84; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 3.8e-66;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 SGGGDLTLGLPSEBEPSPPLAPSEAGSDVDFDGLGMAAGLQSLPTHDSPLQRY 139  
DB 3 SGGGDLTLGLPSEBEPSPPLAPSEAGSDVDFDGLGMAAGLQSLPTHDSPLQRY 62

QY 140 EDPPTVPLPSETDGYVAPLTCSPQ 163  
DB 63 EDPPTVPLPSETDGYVAPLTCSPQ 86

RESULT 5  
US-09-854-356-5  
Sequence 5, Application US/09854356  
Patent No. US20020177567A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Gheyson, Dirk  
APPLICANT: Corixa Corporation  
APPLICANT: SmithKline Beecham Biologicals S. A.  
TITLE OF INVENTION: HER-2/neu Fusion Proteins  
FILE REFERENCE: 014058-009810PC  
CURRENT APPLICATION NUMBER: US/09/854,356  
CURRENT FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: US 09/493,480  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117,976  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5

LENGTH: 59  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
OTHER INFORMATION: portion (delta PD) of human HER-2/neu  
US-09-854-356-5

Query Match 25.1%; Score 59; DB 3; Length 59;  
Best Local Similarity 100.0%; Pred. No. 3.2e-44;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 QNEDGPAASPDLSTYRSLLEDMDGLVDAEYLVPOGFCPPDPAPGAGMVRHR 74  
Db 1 QNEDGPAASPDLSTYRSLLEDMDGLVDAEYLVPOGFCPPDPAPGAGMVRHR 59

RESULT 6  
US-10-425-115-217661

Sequence 217661, Application US/10425115  
Publication No. US20040214272A1

GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 217661

LENGTH: 79  
TYPE: PRT  
ORGANISM: Zea mays

FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_130104C.1.ped  
US-10-425-115-217661

Query Match 19.1%; Score 45; DB 4; Length 79;  
Best Local Similarity 100.0%; Pred. No. 9.8e-32;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AEEYVPOGFCPPDPAPGAGMVRHRSSSTRSGGDLTGL 90  
Db 35 AEEYVPOGFCPPDPAPGAGMVRHRSSSTRSGGDLTGL 79

RESULT 7  
US-09-925-301-1232

Sequence 1232, Application US/09925301  
Patent No. US20020052308A1

GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1232  
LENGTH: 135  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-925-301-1232

Query Match 16.6%; Score 39; DB 3; Length 135;  
Best Local Similarity 100.0%; Pred. No. 3.1e-26;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 KTLSPGKGVKDVFAFGAVENPEYLTPOGAAPORHP 235  
Db 51 KTLSPGKGVKDVFAFGAVENPEYLTPOGAAPORHP 89

RESULT 8  
US-10-484-067-7

Sequence 7, Application US/10484067  
Publication No. US20040241686A1

GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF CALIFORNIA

APPLICANT: NELSON, Edward L.  
TITLE OF INVENTION: HER2/NEU TARGET ANTIGEN AND USE OF SAME TO STIMULATE AN IMMUNE RE  
FILE REFERENCE: UC1170-1

CURRENT APPLICATION NUMBER: US/10/484,067  
CURRENT FILING DATE: 2004-01-15

PRIOR APPLICATION NUMBER: PCT/US02/22975  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: US 60/306,250

PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 7  
LENGTH: 221  
TYPE: PRT

ORGANISM: Rat  
US-10-484-067-7

Query Match 15.7%; Score 37; DB 5; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 RPAATLPERKTLSPGKGVKDVFAFGAVENPEYL 223  
Db 127 RPAATLPERKTLSPGKGVKDVFAFGAVENPEYL 163

RESULT 9  
US-09-354-533-51

Sequence 51, Application US/09354533  
Publication No. US20020055614A1

GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESS: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533

FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031



INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-354-533-51

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDDMGDLVDABEYL 50  
DB 1 EDDDMGDLVDABEYL 15

RESULT 10  
US-09-354-533-52  
Sequence 52, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-354-533-52

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GMAAKGIQSLPTHD 131  
DB 1 GMAAKGIQSLPTHD 15

RESULT 11  
US-09-354-533-53  
Sequence 53, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
Diels, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>

QY 158 TCSPQPEYVNPDPVR 172  
DB 1 TCSPQPEYVNPDPVR 15

RESULT 12  
US-09-354-533-54  
Sequence 54, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Diels, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-09-354-533-54

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLRPKTLSPGKNGV 206  
DB 1 TLRPKTLSPGKNGV 15

RESULT 13  
US-09-354-533-55  
Sequence 55, Application US/09354533  
Publication No. US20020055614A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Daisig, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-354-533-55

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAIVENPEYLTPOGG 228  
DB 1 GGAIVENPEYLTPOGG 15

RESULT 14  
US-10-245-871-581  
Sequence 581, Application US/10245871  
Publication No. US20030235594A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REF-2013  
CURRENT APPLICATION NUMBER: US/10/245,871  
CURRENT FILING DATE: 2003-01-09  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 581  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-245-871-581

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLRPKTLSPGKNGV 206  
DB 1 TLRPKTLSPGKNGV 15

RESULT 15  
US-10-149-138-3722  
Sequence 3722, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esleben  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3722  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3722

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AKGLQSLPTHDPSP 135  
DB 1 AKGLQSLPTHDPSP 15

```
RESULT 16
US-10-149-138-3738
/ Sequence 3738, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bastezan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3738
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3738

Query Match      6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      113 DGDLSGMAKGLQSL 127
DB      1 DGDLSGMAKGLQSL 15

RESULT 17
US-10-149-138-3739
/ Sequence 3739, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bastezan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3739
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3739

Query Match      6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      84 DLTGLPSEBBAVR 98
DB      1 DLTGLPSEBBAVR 15

RESULT 19
US-10-149-138-3743
/ Sequence 3743, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bastezan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3743
/ LENGTH: 15
```

```
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      151 DGYVAPLTCSPQPEY 165
DB      1 DGYVAPLTCSPQPEY 15

RESULT 18
US-10-149-138-3740
/ Sequence 3740, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bastezan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3740
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3740

Query Match      6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      84 DLTGLPSEBBAVR 98
DB      1 DLTGLPSEBBAVR 15

RESULT 19
US-10-149-138-3743
/ Sequence 3743, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bastezan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3743
/ LENGTH: 15
```

APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Esteban

```
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3769
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3769

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      108 GSDVPDGLGMGAAX 122
DB      1 GSDVPDGLGMGAAX 15

RESULT 24
US-10-149-138-3793
/ Sequence 3793, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3793
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3793

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      208 KDVPFAGGAVENPEY 222
DB      1 KDVPFAGGAVENPEY 15

RESULT 25
US-10-149-138-3812
/ Sequence 3812, Application US/10149138
/ Publication No. US20040018971A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3812
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3812

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      135 LQRYSDPTVPLPSE 149
DB      1 LQRYSDPTVPLPSE 15

RESULT 26
US-10-149-138-3813
/ Sequence 3813, Application US/10149138
/ Publication No. US20040018971A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Keogh, Elisea
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to
/ FILE REFERENCE: 2060.0140001
/ CURRENT APPLICATION NUMBER: US/10/149,138
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: PCT/US00/33591
/ PRIOR FILING DATE: 2000-12-11
/ PRIOR APPLICATION NUMBER: US 09/458,299
/ PRIOR FILING DATE: 1999-12-11
/ NUMBER OF SEQ ID NOS: 4641
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3813
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3813

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      124 LQSLPTHDPSLPQRY 138
DB      1 LQSLPTHDPSLPQRY 138
```

Db 1 LQSLPHTDPSPLQRY 15

RESULT 27

US-10-149-138-3832

Sequence 3832, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3832

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3832

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 NEDLGPSPLDSTFY 15

RESULT 28

US-10-149-138-3834

Sequence 3834, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3834

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3834

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 204 NGVYQDVPRFGAVE 218

RESULT 29

US-10-149-138-3845

Sequence 3845, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3845

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3845

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 163 PEVYQDVPRPQPS 177

RESULT 30

US-10-149-138-3854

Sequence 3854, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

PRIOR FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3854

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-3854

SEQ ID NO 3854  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3854

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QGFPCDPAPAGGM 68  
DB 1 QGFPCDPAPAGGM 15

RESULT 31  
US-10-149-138-3858  
Sequence 3858, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3858  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3858

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 QPDVPPQPPSPRBCP 182  
DB 1 QPDVPPQPPSPRBCP 15

RESULT 32  
US-10-149-138-3860  
Sequence 3860, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138

CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3860  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3860

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 QGFPCDPAPAGG 67  
DB 1 QGFPCDPAPAGG 15

RESULT 33  
US-10-149-138-3870  
Sequence 3870, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Bateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3870  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3870

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSLLEDDMDGLVDA 46  
DB 1 RSLLEDDMDGLVDA 15

RESULT 34  
US-10-149-138-3882  
Sequence 3882, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott

APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT FILING DATE: 2002-06-10  
CURRENT APPLICATION NUMBER: US/10/149,138  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3982  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3982

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 TDGYVAPLTCSPQPE 164  
Db 1 TDGYVAPLTCSPQPE 15

RESULT 35  
US-10-149-138-3911  
Sequence 3911, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3911  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3911

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 DLTGLGPESEBAPR 98  
Db 1 DLTGLGPESEBAPR 15

RESULT 36  
US-10-149-138-3916

Sequence 3916, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3916  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3916

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FSRMARDPQRFVVIQ 16  
Db 1 FSRMARDPQRFVVIQ 15

RESULT 37  
US-10-149-138-3917  
Sequence 3917, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3917  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3917

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 12 FVVIQEDLGPAAPL 26  
| | | | | | | | | |  
Db 1 FVVIQEDLGPAAPL 15

## RESULT 38

US-10-149-138-3918  
; Sequence 3918, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Cheenut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3918  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3918

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 GDLVDAEYLVPPQG 55  
| | | | | | | | | |  
Db 1 GDLVDAEYLVPPQG 15

## RESULT 39

US-10-149-138-3923  
; Sequence 3923, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Cheenut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3923  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3923

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 KNGVWDVAFPGAV 217  
| | | | | | | | | |  
Db 1 KNGVWDVAFPGAV 15

## RESULT 40

US-10-149-138-3925  
; Sequence 3925, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Cheenut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3925  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3925

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 LQRYSEDPTVPLPSE 149  
| | | | | | | | | |  
Db 1 LQRYSEDPTVPLPSE 15

## RESULT 41

US-10-149-138-3932  
; Sequence 3932, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Cheenut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3932  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3932

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 QGFPCDPAPGAGM 68  
Db 1 QGFPCDPAPGAGM 15

## RESULT 42

US-10-149-138-3934  
Sequence 3934, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3934  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3934

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 RSLLEDDDMGDLVDA 46  
Db 1 RSLLEDDDMGDLVDA 15

## RESULT 43

US-10-149-138-3935  
Sequence 3935, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
US-10-149-138-3935

FILE REFERENCE: 2060.0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3935  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3935

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 SDVFDGDLGMGAKG 123  
Db 1 SDVFDGDLGMGAKG 15

## RESULT 44

US-10-149-138-3939  
Sequence 3939, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0140001  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3939  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-3939

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 TVPLPSRTGYVAPL 157  
Db 1 TVPLPSRTGYVAPL 15

## RESULT 45

US-10-149-138-3944  
Sequence 3944, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro

```

; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3944
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
; US-10-149-138-3944
```

```

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      31 YRSLEDDDDMGDLVD 45
Db      1 YRSLEDDDDMGDLVD 15
```

```

RESULT 46
US-10-149-138-4486
; Sequence 4486, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4486
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
; US-10-149-138-4486
```

```

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      54 QGFPCPDPAAGAGM 68
Db      1 QGFPCPDPAAGAGM 15
```

```

RESULT 47
US-10-149-138-4487
; Sequence 4487, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4487
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
; US-10-149-138-4487
```

```

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      150 TDGYVAPLTCSPPQE 164
Db      1 TDGYVAPLTCSPPQE 15
```

```

RESULT 48
US-10-149-138-4488
; Sequence 4488, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4488
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
; US-10-149-138-4488
```

```

Query Match          6.4%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 OPDVRRPPSPREGP 162

Db 1 OPDVRRPPSPREGP 15

RESULT 49  
US-10-149-138-4541

/ Sequence 4541, Application US/10149138  
/ Publication No. US20040018971A1

/ GENERAL INFORMATION:

/ APPLICANT: Fikes, John

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Keogh, Elissa

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to

/ FILE REFERENCE: 2060.0140001

/ CURRENT FILING DATE: 2002-06-10

/ PRIOR APPLICATION NUMBER: PCT/US00/33591

/ PRIOR FILING DATE: 2000-12-11

/ PRIOR APPLICATION NUMBER: US 09/458,299

/ PRIOR FILING DATE: 1999-12-11

/ NUMBER OF SEQ ID NOS: 4641

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 4541

/ LENGTH: 15

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Artificial Peptide

US-10-149-138-4541

Query Match 6.4%; Score 15; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FSRMARDPQRFVVIQ 16

Db 1 FSRMARDPQRFVVIQ 15

RESULT 50

US-10-149-138-4542

/ Sequence 4542, Application US/10149138

/ Publication No. US20040018971A1

/ GENERAL INFORMATION:

/ APPLICANT: Fikes, John

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Keogh, Elissa

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to

/ FILE REFERENCE: 2060.0140001

/ CURRENT FILING DATE: 2002-06-10

/ PRIOR APPLICATION NUMBER: PCT/US00/33591

/ PRIOR FILING DATE: 2000-12-11

/ PRIOR APPLICATION NUMBER: US 09/458,299

/ PRIOR FILING DATE: 1999-12-11

/ NUMBER OF SEQ ID NOS: 4641

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 4542

/ LENGTH: 15

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Artificial Peptide

US-10-149-138-4542

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FVVIQEDLGPASPL 26

Db 1 FVVIQEDLGPASPL 15

Search completed: January 18, 2006, 20:59:59  
Job time : 121 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: January 18, 2006, 20:46:59 : Search time 23 Seconds  
(without alignments)  
844.730 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235

Sequence: 1 EFSRMARDPQRFRVYIQNEDL.....AVENPEYLRPGGAAPQHP 235

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 454623

Minimum DB seq length: 0

Maximum DB seq length: 235

## Post-processing: Listing first 200 summaries

## Database :

- Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5 COMB.dep:\*  
2: /cgn2\_6/prodata/1/aa/6 COMB.dep:\*  
3: /cgn2\_6/prodata/1/aa/7 COMB.dep:\*  
4: /cgn2\_6/prodata/1/aa/8 COMB.dep:\*  
5: /cgn2\_6/prodata/1/aa/9 COMB.dep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.dep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	17.4	47	1	US-08-625-322-22
2	22	9.4	47	1	US-08-625-322-23
3	15	6.4	15	1	US-08-467-083-51
4	15	6.4	15	1	US-08-467-083-52
5	15	6.4	15	1	US-08-467-083-53
6	15	6.4	15	1	US-08-467-083-54
7	15	6.4	15	1	US-08-467-083-55
8	15	6.4	15	1	US-08-414-178-51
9	15	6.4	15	1	US-08-414-178-52
10	15	6.4	15	1	US-08-414-178-53
11	15	6.4	15	1	US-08-414-178-54
12	15	6.4	15	1	US-08-414-178-55
13	15	6.4	15	1	US-08-486-348A-51
14	15	6.4	15	1	US-08-486-348A-52
15	15	6.4	15	1	US-08-486-348A-53
16	15	6.4	15	1	US-08-486-348A-54
17	15	6.4	15	1	US-08-486-348A-55
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33	13	5.5	13	2	US-08-403-459-45	Sequence 45, Appl
34	11	4.7	11	2	US-08-625-322-25	Sequence 25, Appl
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36	10	4.3	10	2	US-08-403-459-16	Sequence 16, Appl
37	10	4.3	10	2	US-08-403-459-44	Sequence 44, Appl
38	10	4.3	13	2	US-08-403-459-40	Sequence 40, Appl
39	10	4.3	14	1	US-08-467-083-64	Sequence 64, Appl
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43	10	4.3	14	2	US-08-466-680B-64	Sequence 64, Appl
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45	10	4.3	17	2	US-08-197-484-11	Sequence 11, Appl
46	10	4.3	17	4	PCT-US95-02121-11	Sequence 11, Appl
47	10	4.3	21	1	US-08-423-646A-46	Sequence 46, Appl
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55	9	3.8	9	1	US-08-486-348A-10	Sequence 10, Appl
56	9	3.8	9	1	US-08-486-348A-23	Sequence 23, Appl
57	9	3.8	9	1	US-08-486-348A-24	Sequence 24, Appl
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60	9	3.8	9	1	US-08-468-545B-23	Sequence 23, Appl
61	9	3.8	9	1	US-08-468-545B-24	Sequence 24, Appl
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63	9	3.8	9	1	US-08-159-339A-257	Sequence 257, App
64	9	3.8	9	2	US-08-466-680B-10	Sequence 10, Appl
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67	9	3.8	9	2	US-08-466-680B-25	Sequence 25, Appl
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70	9	3.8	9	2	US-09-354-533-23	Sequence 23, Appl
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73	9	3.8	15	2	US-08-467-083-50	Sequence 50, Appl
74	8	3.4	15	1	US-08-414-178-50	Sequence 50, Appl
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82	7	3.0	11	2	US-08-403-459-37	Sequence 37, Appl
83	7	3.0	14	2	US-08-403-459-38	Sequence 38, Appl
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107	6	2.6	10	2	US-08-594-575C-5	Sequence 5, Appl
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119	6	2.6	14	1	US-08-468-545B-65	Sequence 65, Appl
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126	6	2.6	26	1	US-08-484-631-90	Sequence 90, Appl
127	6	2.6	26	1	US-08-827-570-90	Sequence 90, Appl
128	6	2.6	28	1	US-08-220-378-8	Sequence 8, Appl
129	6	2.6	28	1	US-08-696-012-8	Sequence 8, Appl
130	6	2.6	29	2	US-09-579-181-8	Sequence 8, Appl
131	6	2.6	34	1	US-08-085-122-11	Sequence 11, Appl
132	6	2.6	34	1	US-08-319-052-21	Sequence 21, Appl
133	6	2.6	34	2	US-08-442-108B-21	Sequence 21, Appl
134	6	2.6	36	2	US-08-856-074A-32	Sequence 32, Appl
135	6	2.6	37	1	US-08-448-481-2	Sequence 2, Appl
136	6	2.6	41	2	US-08-856-074A-31	Sequence 31, Appl
137	6	2.6	46	2	US-08-856-074A-30	Sequence 30, Appl
138	6	2.6	46	2	US-08-856-074A-39	Sequence 39, Appl
139	6	2.6	48	1	US-08-825-322-24	Sequence 24, Appl
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141	6	2.6	55	2	US-09-513-999C-4427	Sequence 4427, Ap
142	6	2.6	57	2	US-09-513-999C-4630	Sequence 4630, Ap
143	6	2.6	57	2	US-09-513-999C-6396	Sequence 6396, Ap
144	6	2.6	59	2	US-09-205-258-1114	Sequence 1114, Ap
145	6	2.6	59	2	US-10-004-860-1114	Sequence 1114, Ap
146	6	2.6	60	2	US-08-856-074A-1	Sequence 1, Appl
147	6	2.6	60	2	US-09-270-767-60124	Sequence 60124, A
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153	6	2.6	71	2	US-09-902-540-16565	Sequence 16565, A
154	6	2.6	72	2	US-09-489-039A-14236	Sequence 14236, A
155	6	2.6	73	2	US-09-513-999C-5640	Sequence 5640, Ap
156	6	2.6	76	2	US-09-621-976-7097	Sequence 7097, Ap
157	6	2.6	79	1	US-08-469-412A-12	Sequence 12, Appl
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160	6	2.6	84	2	US-09-270-767-58538	Sequence 58538, A
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163	6	2.6	85	2	US-10-004-860-1161	Sequence 1161, Ap
164	6	2.6	86	2	US-09-178-093B-43	Sequence 43, Appl
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167	6	2.6	92	2	US-09-513-999C-6337	Sequence 6337, Ap
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169	6	2.6	95	2	US-09-198-452A-256	Sequence 256, App
170	6	2.6	98	2	US-09-252-991A-30584	Sequence 30584, A
171	6	2.6	99	1	US-08-795-444-1	Sequence 1, Appl
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173	6	2.6	100	1	US-08-278-089A-29	Sequence 29, Appl

174	6	2.6	100	1	US-08-838-957A-28	Sequence 28, Appl
175	6	2.6	105	2	US-09-727-739B-36	Sequence 36, Appl
176	6	2.6	106	2	US-09-248-796A-15942	Sequence 15942, A
177	6	2.6	109	2	US-09-270-767-40248	Sequence 40248, A
178	6	2.6	109	2	US-09-270-767-55464	Sequence 55464, A
179	6	2.6	111	2	US-09-252-991A-20456	Sequence 20456, A
180	6	2.6	112	2	US-09-605-703B-2024	Sequence 2024, Ap
181	6	2.6	115	2	US-09-489-039A-13083	Sequence 13083, A
182	6	2.6	116	2	US-09-543-681A-6137	Sequence 6137, Ap
183	6	2.6	117	2	US-09-270-767-36131	Sequence 36131, A
184	6	2.6	117	2	US-09-270-767-51348	Sequence 51348, A
185	6	2.6	117	2	US-10-104-047-3312	Sequence 3312, Ap
186	6	2.6	118	2	US-09-640-211A-661	Sequence 661, App
187	6	2.6	120	2	US-09-621-976-7098	Sequence 7098, Ap
188	6	2.6	122	2	US-09-252-991A-24014	Sequence 24014, A
189	6	2.6	122	2	US-09-252-991A-25805	Sequence 25805, A
190	6	2.6	122	2	US-09-489-039A-8571	Sequence 8571, Ap
191	6	2.6	123	2	US-09-328-352-4127	Sequence 4127, Ap
192	6	2.6	123	2	US-09-248-796A-18549	Sequence 18549, A
193	6	2.6	124	2	US-09-640-211A-1124	Sequence 1124, Ap
194	6	2.6	124	2	US-10-104-047-2155	Sequence 2155, A
195	6	2.6	125	2	US-09-252-991A-24005	Sequence 24005, A
196	6	2.6	127	2	US-09-173-300-40	Sequence 40, Appl
197	6	2.6	127	2	US-10-027-450-40	Sequence 40, Appl
198	6	2.6	129	2	US-09-252-991A-22436	Sequence 22436, A
199	6	2.6	131	2	US-09-252-991A-30854	Sequence 30854, A
200	6	2.6	131	2	US-09-270-767-31762	Sequence 31762, A

RESULT 1  
US-08-625-322-22  
Sequence 22, Application US/08625322  
Patent No. 5804412  
GENERAL INFORMATION:  
APPLICANT: GILL, Gordon N.  
APPLICANT: KURTEN, Richard C.  
APPLICANT: CEDENA, Deborah L.  
TITLE OF INVENTION: Sorting Nexins and Methods of Using Same  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/625,322  
FILING DATE: 01-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1955  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-625-322-22

Query Match 17.4%, Score 41, DB 1, Length 47,

Best Local Similarity 100.0%; Pred. No. 3.4e-31;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRMDPQRFVIVQNEIDGSPASPLDSTFRSLLEDDMG 41  
Db 7 EFSRMDPQRFVIVQNEIDGSPASPLDSTFRSLLEDDMG 47

## RESULT 2

US-08-625-322-23  
Sequence 23, Application US/08625322

Patent No. 5804412  
GENERAL INFORMATION:

APPLICANT: Gill, Gordon N.  
APPLICANT: Kuten, Richard C.  
APPLICANT: Cadena, Deborah L.  
TITLE OF INVENTION: Sorting Nexins and Methods of Using Same  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/625,322  
FILING DATE: 01-APR-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1955

TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 47 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-625-322-23

Query Match 9.4%; Score 22; DB 1; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.6e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFSRMDPQRFVIVQNEIDGSP 22  
Db 7 EFSRMDPQRFVIVQNEIDGSP 28

## RESULT 3

US-08-467-083-51

Sequence 51, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:

ADDRESSER: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

US-08-467-083-51

COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

TELEX: 3723836 SEBDAHBRYX  
INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-467-083-51

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 EDDMGDLVDABERYL 50  
Db 1 EDDMGDLVDABERYL 15

## RESULT 4

US-08-467-083-52

Sequence 52, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:

ADDRESSER: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

ZIP: 98104-7092  
COUNTRY: US

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

TELEX: 3723836 SEBDAHBRYX  
INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GMAKGLQSLPTHD 131  
DB 1 GMAKGLQSLPTHD 15

## RESULT 5

US-08-467-083-53  
Sequence 53, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disib, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPEYVNOPDVR 172  
DB 1 TCSPEYVNOPDVR 15

RESULT 6  
US-08-467-083-54  
Sequence 54, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disib, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-54

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPRTLSPGKGV 206  
DB 1 TLERPRTLSPGKGV 15

RESULT 7  
US-08-467-083-55  
Sequence 55, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disib, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-55



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERY  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-55

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAIVENPEYLTPOGG 228  
DB 1 GGAIVENPEYLTPOGG 15

RESULT 8  
US-08-414-417B-51  
Sequence 51, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERY  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-MAR-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERY  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
US-08-414-417B-51  
Sequence 52, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERY  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-414-417B-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDMGDLVDAREYL 50  
DB 1 EDDMGDLVDAREYL 15

RESULT 9  
US-08-414-417B-52  
Sequence 52, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERY  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-414-417B-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GGAAGKGLSLPTHD 131  
DB 1 GGAAGKGLSLPTHD 15

RESULT 10  
US-08-414-417B-53  
Sequence 53, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDANBERY  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Seed and Berry LLP  
;/ STREET: 6300 Columbia Center, 701 Fifth Avenue  
;/ CITY: Seattle  
;/ STATE: Washington  
;/ COUNTRY: US  
;/ ZIP: 98104-7092  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patentin Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/414,417B  
;/ FILING DATE: 31-MAR-1995  
;/ CLASSIFICATION: 424  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Sharkey, Richard G.  
;/ REGISTRATION NUMBER: 32,629  
;/ REFERENCE/DOCKET NUMBER: 920010.448C2  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (206) 622-4900  
;/ TELEFAX: (206) 682-6031  
;/ INFORMATION FOR SEQ ID NO: 53:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ US-08-414-417B-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNOQDVR 172  
DB 1 TCSPQPEYVNOQDVR 15  
|||||

RESULT 11  
US-08-414-417B-54  
/ Sequence 54, Application US/08414417B  
/ Patent No. 5801005  
/ GENERAL INFORMATION:  
/ APPLICANT: Cheever, Martin A.  
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Seed and Berry LLP  
/ STREET: 6300 Columbia Center, 701 Fifth Avenue  
/ CITY: Seattle  
/ STATE: Washington  
/ COUNTRY: US  
/ ZIP: 98104-7092  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/414,417B  
/ FILING DATE: 31-MAR-1995  
/ CLASSIFICATION: 424  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Sharkey, Richard G.  
/ REGISTRATION NUMBER: 32,629  
/ REFERENCE/DOCKET NUMBER: 920010.448C2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (206) 622-4900  
/ TELEFAX: (206) 682-6031

;/ INFORMATION FOR SEQ ID NO: 54:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ US-08-414-417B-54

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPKTISPRKNGV 206  
DB 1 TLERPKTISPRKNGV 15  
|||||

RESULT 12  
US-08-414-417B-55  
/ Sequence 55, Application US/08414417B  
/ Patent No. 5801005  
/ GENERAL INFORMATION:  
/ APPLICANT: Cheever, Martin A.  
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Seed and Berry LLP  
/ STREET: 6300 Columbia Center, 701 Fifth Avenue  
/ CITY: Seattle  
/ STATE: Washington  
/ COUNTRY: US  
/ ZIP: 98104-7092  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/414,417B  
/ FILING DATE: 31-MAR-1995  
/ CLASSIFICATION: 424  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Sharkey, Richard G.  
/ REGISTRATION NUMBER: 32,629  
/ REFERENCE/DOCKET NUMBER: 920010.448C2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (206) 622-4900  
/ TELEFAX: (206) 682-6031  
/ INFORMATION FOR SEQ ID NO: 55:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
;/ US-08-414-417B-55

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAIVENPEYLTPOGG 228  
DB 1 GGAIVENPEYLTPOGG 15  
|||||

RESULT 13  
US-08-486-348A-51  
/ Sequence 51, Application US/08486348A  
/ Patent No. 5846538  
/ GENERAL INFORMATION:  
/ APPLICANT: Cheever, Martin A.  
/ APPLICANT: Distis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,348A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-6031  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-51

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDMDGLVDAEYL 50  
DB 1 EDDMDGLVDAEYL 15

RESULT 14  
US-08-486-348A-52  
Sequence 52, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
ATTORNEY/AGENT INFORMATION:  
NAME: Disla, Mary L.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNPQDVR 172  
DB 1 TCSPQPEYVNPQDVR 15

RESULT 16  
US-08-486-348A-54  
Sequence 54, Application US/08486348A

REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GMGAAGLQSLPPTH 131  
DB 1 GMGAAGLQSLPPTH 15

RESULT 15  
US-08-486-348A-53  
Sequence 53, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
ATTORNEY/AGENT INFORMATION:  
NAME: Disla, Mary L.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-486-348A-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNPQDVR 172  
DB 1 TCSPQPEYVNPQDVR 15

RESULT 16  
US-08-486-348A-54  
Sequence 54, Application US/08486348A

```
/ Patent No. 5846538
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disib, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,348A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C6
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-486-348A-54

Query Match 6.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPRTLSPGKNGV 206
DB 1 TLERPRTLSPGKNGV 15

RESULT 17
US-08-486-348A-55
/ Sequence 55, Application US/08486348A
/ Patent No. 5846538
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disib, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,348A
/ FILING DATE: 07-JUN-1995
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/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C6
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-486-348A-55

Query Match 6.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAVENPEYLTPOGG 228
DB 1 GGAVENPEYLTPOGG 15

RESULT 18
US-08-468-545B-51
/ Sequence 51, Application US/08468545B
/ Patent No. 5876712
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disib, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,545B
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-468-545B-51

Query Match 6.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EDDMGDLVDABEYL 50
DB 1 EDDMGDLVDABEYL 15
```

RESULT 19  
US-08-468-545B-52  
Sequence 52, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-52

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GNGAKGLQSLPTHD 131  
DB 1 GNGAKGLQSLPTHD 15

RESULT 20  
US-08-468-545B-53  
Sequence 53, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-53

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPOPEYVNPQDVR 172  
DB 1 TCSPOPEYVNPQDVR 15

RESULT 21  
US-08-468-545B-54  
Sequence 54, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION/DOCKET NUMBER: 32,629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-54

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 TLERPKTSPGKNGV 206  
|||||  
Db 1 TLERPKTSPGKNGV 15

## RESULT 22

US-08-466-545B-55  
; Sequence 55, Application US/08466545B  
; Patent No. 5876712  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Diels, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,545B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-466-545B-55

Query Match 6.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 214 GGAVNPEYLTPOGG 228  
|||||  
Db 1 GGAVNPEYLTPOGG 15

RESULT 23  
US-08-466-680B-51  
; Sequence 51, Application US/08466680B  
; Patent No. 6075122  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Diels, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,680B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-466-680B-51

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EDDMGDLVDAEYTL 50  
|||||  
Db 1 EDDMGDLVDAEYTL 15

RESULT 24  
US-08-466-680B-52  
; Sequence 52, Application US/08466680B  
; Patent No. 6075122  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Diels, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,680B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-466-680B-52

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GNGAKGLOSLPTHD 131  
DB 1 GNGAKGLOSLPTHD 15

RESULT 25  
US-08-466-680B-53

Sequence 53, Application US/08466680B  
Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disls, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-466-680B-53

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPOPEYVNOQDVR 172  
DB 1 TCSPOPEYVNOQDVR 15

RESULT 26  
US-08-466-680B-54

Sequence 54, Application US/08466680B

Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disls, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle  
STATE: Washington  
COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-466-680B-54

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLERPKTSLPGKNGV 206  
DB 1 TLERPKTSLPGKNGV 15

RESULT 27  
US-08-466-680B-55

Sequence 55, Application US/08466680B

Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disls, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
US-08-466-680B-55

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 GGAVENPEYLTPOGG 228  
Db 1 GGAVENPEYLTPOGG 15

RESULT 28  
US-09-354-533-51  
Sequence 51, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Diels, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-354-533-51

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 EDDMDGLVDABEYL 50  
Db 1 EDDMDGLVDABEYL 15

RESULT 29  
US-09-354-533-52  
Sequence 52, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Diels, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9

US-09-354-533-52

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 GMAAKGLQSLPTH 131  
Db 1 GMAAKGLQSLPTH 15

RESULT 30  
US-09-354-533-53  
Sequence 53, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
Diels, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 53:  
US-09-354-533-53

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 TCSPQPEYVNPQDVR 172  
DB 1 TCSPQPEYVNPQDVR 15

RESULT 31  
US-09-354-533-54  
Sequence 54, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-09-354-533-54

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLSPKTLSPKNGV 206  
DB 1 TLSPKTLSPKNGV 15

RESULT 32  
US-09-354-533-55

Sequence 55, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-09-354-533-55

Query Match 6.4%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GGAVENPEYLTPOGG 228  
DB 1 GGAVENPEYLTPOGG 15

RESULT 33  
US-08-403-459-45  
Sequence 45, Application US/08403459  
Patent No. 651942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantine G.  
APPLICANT: Isk, Bryan A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-45

Query Match 5.5%; Score 13; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 PDGDLGMGAAGL 124  
Db 1 PDGDLGMGAAGL 13

RESULT 34  
US-08-625-322-25  
Sequence 25, Application US/08625322  
Patent No. 5804412  
GENERAL INFORMATION:  
APPLICANT: G11, Gordon N.  
APPLICANT: Kuten, Richard C.  
APPLICANT: Cadena, Deborah L.  
TITLE OF INVENTION: Sorting Nexins and Methods of Using Same  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/625,322  
FILING DATE: 01-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,915  
REFERENCE/DOCKET NUMBER: P-UD 1955  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-625-322-25

Query Match 4.7%; Score 11; DB 1; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.0059;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRWARDPOR 11  
Db 7 EFSRWARDPOR 17

RESULT 35  
US-08-159-339A-268  
Sequence 268, Application US/08159339A  
Patent No. 6037135  
GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard W.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Eilen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 268:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-268

Query Match 4.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 MGDVDAEY 49  
Db 1 MGDVDAEY 10

RESULT 36  
US-08-403-459-16  
Sequence 16, Application US/08403459  
Patent No. 6514942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantin G.  
APPLICANT: Fisk, Bryan A.

APPLICANT: Ioannides, Maria G.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
TITLE OF INVENTION: T-LYMPHOCYTES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-16

Query Match 4.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 115 DLGMAAKGL 124  
DB 1 DLGMAAKGL 10

RESULT 37  
US-08-403-459-44  
Sequence 44: Application US/08403459  
Patent No. 6514942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantin G.  
APPLICANT: Fisk, Bryan A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
TITLE OF INVENTION: T-LYMPHOCYTES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-44

Query Match 4.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 115 DLGMAAKGL 124  
DB 1 DLGMAAKGL 10

RESULT 38  
US-08-403-459-40  
Sequence 40: Application US/08403459  
Patent No. 6514942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantin G.  
APPLICANT: Fisk, Bryan A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
TITLE OF INVENTION: T-LYMPHOCYTES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-40

Query Match 4.3%; Score 10; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EFSRWARDPQ 10  
|||||||  
Db 4 EFSRWARDPQ 13

## RESULT 39

US-08-467-083-64  
; Sequence 64, Application US/08467083  
; Patent No. 5726023

## GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disib, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEFAX: 3723836 SEEDANBERRY

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-467-083-64

Query Match 4.3%; Score 10; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EFSRWARDPQ 10

|||||||

Db 5 EFSRWARDPQ 14

RESULT 40

US-08-414-417B-64

; Sequence 64, Application US/08414417B

; Patent No. 5801005

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disib, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

ADDRESS: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,417B

FILING DATE: 31-MAR-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-414-417B-64

Query Match 4.3%; Score 10; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EFSRWARDPQ 10

|||||||

Db 5 EFSRWARDPQ 14

RESULT 41

US-08-486-348A-64

; Sequence 64, Application US/08486348A

; Patent No. 5846338

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disib, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,348A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-468-348A-64

Query Match 4.3%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMAPDQ 10  
Db 5 EFSRMAPDQ 14

RESULT 42  
US-08-468-545B-64  
Sequence 64, Application US/08468545B  
Patent No. 5876712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448CS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-468-545B-64

Query Match 4.3%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMAPDQ 10  
Db 5 EFSRMAPDQ 14

RESULT 43  
US-08-466-680B-64  
Sequence 64, Application US/08466680B  
Patent No. 6075122  
GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-466-680B-64

Query Match 4.3%; Score 10; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFSRMAPDQ 10  
Db 5 EFSRMAPDQ 14

RESULT 44  
US-09-354-533-64  
Sequence 64, Application US/09354533  
Patent No. 6664370  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-JUL-1999  
CLASSIFICATION: <Unknown>

```
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-354-533-64

Query Match      4.3%; Score 10; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EFSRWARDPQ 10
Db      5 EFSRWARDPQ 14

RESULT 45
US-08-197-484-11
Sequence 11, Application US/08197484
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Eateban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-11

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Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EFSRWARDPQ 10
Db      8 EFSRWARDPQ 17

RESULT 46
PCT-US95-02121-11
Sequence 11, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-11

Query Match      4.3%; Score 10; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EFSRWARDPQ 10
Db      8 EFSRWARDPQ 17
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RESULT 47  
US-08-423-646A-46  
Sequence 46, Application US/08423646A  
Patent No. 6280964  
GENERAL INFORMATION:  
APPLICANT: Kavanaugh, William M.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: Binding Sites for Phosphotyrosine  
TITLE OF INVENTION: Binding Domains  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/423,646A  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-059100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: one-of(11)  
OTHER INFORMATION: /note="Xaa is phosphotyrosine."  
US-08-423-646A-46

Query Match 4.3%; Score 10; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AFGGAVENPE 221  
DB 1 AFGGAVENPE 10

RESULT 48  
US-08-467-083-10  
Sequence 10, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disla, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEDBANBRY  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-10

Query Match 3.8%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TISPGKGV 206  
DB 1 TISPGKGV 9

RESULT 49  
US-08-467-083-23  
Sequence 23, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disla, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:

Search completed: January 19, 2006, 20:50:09  
Job time : 31 secs

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELETYPE: 3723836 SEEDANBERY  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-23

Query Match 3.8%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DLVDAEYL 50  
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Db 1 DLVDAEYL 9

RESULT 50  
US-08-467-083-24  
Sequence 24, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disig, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELETYPE: 3723836 SEEDANBERY  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-24

Query Match 3.8%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 GLPSEEEA 96  
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Db 1 GLPSEEEA 9



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OM protein - protein search, using SW model

Run on: January 18, 2006, 20:49:47 : Search time 30 Seconds  
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Gapop 60.0, Gapext 60.0

Searched: 70606 seqs, 10133881 residues

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Total number of hits satisfying chosen parameters: 54762

Minimum DB seq length: 0  
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Post-processing: Listing first 200 summaries

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Published Applications AA New:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARYS

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6	9	3.8	9	US-11-033-039-607	Sequence 607, App
7	9	3.8	14	US-11-033-039-589	Sequence 589, App
8	9	3.8	14	US-11-033-039-593	Sequence 593, App
9	7	3.0	12	US-11-033-039-575	Sequence 575, App
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11	7	3.0	216	US-11-186-284-217	Sequence 217, App
12	6	2.6	9	US-11-033-039-586	Sequence 586, App
13	6	2.6	10	US-11-057-708-25	Sequence 25, App
14	6	2.6	14	US-11-033-039-594	Sequence 594, App
15	6	2.6	112	US-10-510-386-140	Sequence 140, App
16	6	2.6	122	US-09-978-360A-604	Sequence 604, App
17	6	2.6	147	US-10-793-626-2502	Sequence 2502, App
18	6	2.6	156	US-10-467-657-112	Sequence 112, App
19	6	2.6	156	US-10-467-657-8550	Sequence 8550, App
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22	5	2.1	8	US-11-045-024-1111	Sequence 1111, App
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34	5	2.1	10	US-11-045-024-9197	Sequence 9197, App
35	5	2.1	10	US-11-062-186-128	Sequence 128, App
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38	5	2.1	11	US-11-058-735-69	Sequence 69, App
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41	5	2.1	11	US-11-045-024-4215	Sequence 4215, App
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151 5 2.1 134 6 US-10-986-501-199 Sequence 199, App
152 5 2.1 134 6 US-10-875-800-2 Sequence 2, Appli
153 5 2.1 134 7 US-11-043-590-12 Sequence 12, Appli
154 5 2.1 135 6 US-10-821-234-1018 Sequence 1018, App
155 5 2.1 137 5 US-09-978-360A-765 Sequence 765, App
156 5 2.1 138 6 US-10-789-273-4 Sequence 4, Appli
157 5 2.1 138 6 US-10-789-273-8 Sequence 8, Appli
158 5 2.1 138 6 US-10-789-273-12 Sequence 12, Appli
159 5 2.1 138 6 US-10-527-500-15 Sequence 15, Appli
160 5 2.1 140 6 US-10-055-877-331 Sequence 331, App
161 5 2.1 140 6 US-10-055-877-333 Sequence 333, App
162 5 2.1 140 6 US-10-055-877-334 Sequence 334, App
163 5 2.1 140 7 US-11-193-512-27 Sequence 27, Appli
164 5 2.1 141 7 US-11-119-098-1 Sequence 1, Appli
165 5 2.1 142 6 US-10-793-626-3038 Sequence 3038, App
166 5 2.1 142 7 US-11-055-822-64 Sequence 64, Appli
167 5 2.1 142 7 US-11-186-284-105 Sequence 105, App
168 5 2.1 143 6 US-10-467-657-274 Sequence 274, App
169 5 2.1 143 6 US-10-467-657-3720 Sequence 3720, App
170 5 2.1 143 7 US-11-116-144-166 Sequence 166, App
171 5 2.1 144 6 US-10-821-234-1254 Sequence 1254, App
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172 5 2.1 145 6 US-10-467-657-6506 Sequence 6506, App
173 5 2.1 145 7 US-11-215-721-3 Sequence 3, Appli
174 5 2.1 146 6 US-10-793-626-2694 Sequence 2694, App
175 5 2.1 146 7 US-11-083-800-8 Sequence 8, Appli
176 5 2.1 148 6 US-10-793-626-824 Sequence 824, App
177 5 2.1 148 7 US-11-055-822-1076 Sequence 1076, App
178 5 2.1 149 6 US-10-467-657-270 Sequence 270, App
179 5 2.1 149 6 US-10-467-657-3668 Sequence 3668, App
180 5 2.1 150 7 US-11-152-497-4 Sequence 4, Appli
181 5 2.1 152 6 US-10-994-820A-13 Sequence 13, Appli
182 5 2.1 152 6 US-10-467-657-4310 Sequence 4310, App
183 5 2.1 152 7 US-11-152-497-6 Sequence 6, Appli
184 5 2.1 153 5 US-09-978-360A-490 Sequence 490, App
185 5 2.1 153 5 US-09-978-360A-760 Sequence 760, App
186 5 2.1 154 6 US-10-821-234-1469 Sequence 1469, App
187 5 2.1 155 6 US-10-793-626-2990 Sequence 2990, App
188 5 2.1 155 6 US-10-467-657-4490 Sequence 4490, App
189 5 2.1 155 7 US-11-116-144-159 Sequence 159, App
190 5 2.1 156 6 US-10-821-234-1424 Sequence 1424, App
191 5 2.1 156 7 US-11-116-144-31 Sequence 31, Appli
192 5 2.1 156 7 US-11-116-144-168 Sequence 168, App
193 5 2.1 157 6 US-10-994-820A-14 Sequence 14, Appli
194 5 2.1 158 6 US-10-995-561-585 Sequence 585, App
195 5 2.1 158 6 US-10-995-561-586 Sequence 586, App
196 5 2.1 158 7 US-11-157-049-40 Sequence 40, Appli
197 5 2.1 158 6 US-10-793-626-940 Sequence 940, App
198 5 2.1 160 7 US-11-157-049-23 Sequence 23, Appli
199 5 2.1 160 7 US-11-157-049-39 Sequence 39, Appli
200 5 2.1 160 7 US-11-215-721-1 Sequence 1, Appli
```

## ALIGNMENTS

```
RESULT 1
US-11-033-039-581
; Sequence 581, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 581
; TYPE: PRT
; LENGTH: 15
; ORGANISM: Homo sapiens
US-11-033-039-581

Query Match 6.4%, Score 15, DB 7, Length 15,
Best Local Similarity 100.0%, Pred. No. 1.5e-08,
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TLRPKTLSPGKNGV 206
Db 1 TLRPKTLSPGKNGV 15

RESULT 2
US-11-033-039-574
; Sequence 574, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
```

```

; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 574
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-574
```

```

Query Match          5.1%; Score 12; DB 7; Length 12;
Best Local Similarity 100.0%; Pred.No. 1.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EFRRMARDPQRF 12
      |||||
Db      1 EFRRMARDPQRF 12
```

```

RESULT 3
US-11-033-039-584
; Sequence 584, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 584
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-584
```

```

Query Match          4.3%; Score 10; DB 7; Length 14;
Best Local Similarity 100.0%; Pred.No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EFRRMARDPQ 10
      |||||
Db      5 EFRRMARDPQ 14
```

```

RESULT 4
US-11-033-039-554
; Sequence 554, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
```

```

; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 554
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-554
```

```

Query Match          3.8%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred.No. 5.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      12 FVVIQNEDL 20
      |||||
Db      1 FVVIQNEDL 9
```

```

RESULT 5
US-11-033-039-560
; Sequence 560, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 560
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-560
```

```

Query Match          3.8%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred.No. 5.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      68 MVYHRRSS 76
      |||||
Db      1 MVYHRRSS 9
```

```

RESULT 6
US-11-033-039-607
; Sequence 607, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
```

PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 607  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-607

Query Match 3.8%; Score 9; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 EYLVPQOGF 56  
Db 1 EYLVPQOGF 9

RESULT 7  
US-11-033-039-589  
Sequence 589, Application US/11033039  
Publication No. US20060002947A1

GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 589  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: Ava  
US-11-033-039-589

Query Match 3.8%; Score 9; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FVVIQNEDL 20  
Db 6 FVVIQNEDL 14

RESULT 8  
US-11-033-039-593

Sequence 593, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 593  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: Ava  
US-11-033-039-593

Query Match 3.8%; Score 9; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 MVHRHRSS 76  
Db 6 MVHRHRSS 14

RESULT 9  
US-11-033-039-575  
Sequence 575, Application US/11033039  
Publication No. US20060002947A1

GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 575  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-575

Query Match 3.0%; Score 7; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 FDGDLGM 118  
Db 1 FDGDLGM 7

RESULT 10  
US-10-467-657-1338

Sequence 1338, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIAGNI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GOMOCOCCAL PROTEINS AND NUCLEIC ACIDS

```
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO: 1338
LENGTH: 161
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1338

Query Match      3.0%; Score 7; DB 6; Length 161;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      141 DPTVPLP 147
DB      129 DPTVPLP 135

RESULT 11
US-11-186-284-217
Sequence 217, Application US/11/186,284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangt
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPW01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 217
LENGTH: 216
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-217

Query Match      3.0%; Score 7; DB 7; Length 216;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      98 RSPPLAP 104
DB      206 RSPPLAP 212

RESULT 12
US-11-033-039-586
Sequence 586, Application US/11/033,039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
```

```
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 586
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-11-033-039-586

Query Match      2.6%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EFSRMA 6
DB      4 EFSRMA 9

RESULT 13
US-11-057-708-25
Sequence 25, Application US/11/057,708
Publication No. US20050250702A1
GENERAL INFORMATION:
APPLICANT: Universiteit Utrecht
APPLICANT: Strous, Gerardus
APPLICANT: Van Kerkhof, Petrus
APPLICANT: Govers, Roland
TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEAS
TITLE OF INVENTION: INHIBITORS OR RECEPTOR FRAGMENTS
FILE REFERENCE: 2183-4525US
CURRENT APPLICATION NUMBER: US/11/057,708
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: US/09/660,302
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: PCT/NL99/00136
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: EP98200799.9
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 25
LENGTH: 10
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Uneure, ERB2 TKR (neu-oncogene)
US-11-057-708-25

Query Match      2.6%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      218 ENPEYL 223
DB      1 ENPEYL 6

RESULT 14
US-11-033-039-594
Sequence 594, Application US/11/033,039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
```

```
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REF-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 594
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ FEATURE:
/ OTHER INFORMATION: hybrid peptide
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-594

Query Match          2.6%; Score 6; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EFSRMA 6
        |||||
        9 EFSRMA 14

RESULT 15
US-10-510-386-140
/ Sequence 140, Application US/10510386
/ Publication No. US20050244922A1
/ GENERAL INFORMATION:
/ APPLICANT: Andersen, Jens Toume
/ APPLICANT: Clausen, Id Groth
/ APPLICANT: Jorgensen, Steen Tyroels
/ APPLICANT: Olsen, Peter Bjarkle
/ APPLICANT: Rasmussen, Michael Dolberg
/ TITLE OF INVENTION: Improved Bacillus Host Cell
/ FILE REFERENCE: 10294,204-US
/ CURRENT APPLICATION NUMBER: US/10/510,386
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 248
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 140
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-10-510-386-140

Query Match          2.6%; Score 6; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 TRSGG 83
        |||||
        105 TRSGG 110

RESULT 16
US-09-978-360A-604
/ Sequence 604, Application US/09978360A
/ Publication No. US20060009633A9
/ GENERAL INFORMATION:
/ APPLICANT: Edwards, Jean-Baptiste Dumas Milne
/ APPLICANT: Duclet, Aymeric
/ APPLICANT: Bougueleret, Lydie
```

```
/ APPLICANT: Jobert, Severin
/ APPLICANT: Clusel, Catherine
/ TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
/ FILE REFERENCE: 56 US4, CIP
/ CURRENT APPLICATION NUMBER: US/09/978,360A
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: US 60/066,677
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: US 60/069,957
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: US 60/074,121
/ PRIOR FILING DATE: 1998-02-09
/ PRIOR APPLICATION NUMBER: US 60/081,563
/ PRIOR FILING DATE: 1998-04-13
/ PRIOR APPLICATION NUMBER: US 60/096,116
/ PRIOR FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: US 60/099,273
/ PRIOR FILING DATE: -03-04
/ PRIOR APPLICATION NUMBER: US 09/191,997
/ PRIOR FILING DATE: 1998-11-13
/ PRIOR APPLICATION NUMBER: US 09/215,435
/ PRIOR FILING DATE: 1998-12-17
/ PRIOR APPLICATION NUMBER: PCT/IB98/02122
/ PRIOR FILING DATE: 1998-12-17
/ PRIOR APPLICATION NUMBER: US 09/247,155
/ PRIOR FILING DATE: 1999-02-09
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 810
/ SOFTWARE: Patent.pm
/ SEQ ID NO 604
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: -56...-1
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (-13, 4)
/ OTHER INFORMATION: unknown
US-09-978-360A-604

Query Match          2.6%; Score 6; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      127 LPTHP 132
        |||||
        22 LPTHP 27

RESULT 17
US-10-793-626-2502
/ Sequence 2502, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PUS480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2502
/ LENGTH: 147
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-2502
```

Query Match 2.6%; Score 6; DB 6; Length 147;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 PSEER 95  
|||||  
Db 112 PSEER 117

RESULT 18  
US-10-467-657-112  
; Sequence 112, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 112  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-112

Query Match 2.6%; Score 6; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 EGAGSD 110  
|||||  
Db 73 EGAGSD 78

RESULT 19  
US-10-467-657-8550  
; Sequence 8550, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8550  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8550

Query Match 2.6%; Score 6; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 EGAGSD 110  
|||||

Db 73 EGAGSD 78

RESULT 20  
US-10-995-561-563  
; Sequence 563, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 563  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-563

Query Match 2.6%; Score 6; DB 6; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 PSEER 96  
|||||  
Db 167 PSEER 172

RESULT 21  
US-11-022-562-226  
; Sequence 226, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruprecht, Ruth M.  
; APPLICANT: Shienog, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-022-562-226

Query Match 2.6%; Score 6; DB 7; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 SDVFDG 114  
|||||  
Db 172 SDVFDG 177

RESULT 22  
US-11-045-024-1111  
; Sequence 1111, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott

APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esreban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1111  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1111

Query Match 2.1%; Score 5; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 1 GATLE 5

RESULT 23  
US-11-045-024-6406  
Sequence 6406, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esreban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6406  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-6406

Query Match 2.1%; Score 5; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 1 GATLE 5

RESULT 24  
US-11-062-186-2  
Sequence 2, Application US/11062186  
Publication No. US20050272097A1  
GENERAL INFORMATION:  
APPLICANT: CALENOFF, EMANUEL  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
FILE REFERENCE: 21417-98470  
CURRENT APPLICATION NUMBER: US/11/062,186  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: 60/546,062  
PRIOR FILING DATE: 2004-02-18  
PRIOR APPLICATION NUMBER: 60/545,980  
PRIOR FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-062-186-2

Query Match 2.1%; Score 5; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 SPGRN 204  
Db 2 SPGRN 6

RESULT 25  
US-10-467-657-4572  
Sequence 4572, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASTRONI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12



NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMin99, version 1.04  
SEQ ID NO: 4572  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4572

Query Match 2.1%; Score 5; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 GAGGM 68  
Db 4 GAGGM 8

RESULT 26  
US-11-045-024-1231  
Sequence 1231, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1231  
LENGTH: 9  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1231

Query Match 2.1%; Score 5; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 1 GATLE 5

RESULT 27  
US-11-045-024-5189  
Sequence 5189, Application US/11045024

Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 5189  
LENGTH: 9  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5189

Query Match 2.1%; Score 5; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 GATLE 194  
Db 3 GATLE 7

RESULT 28  
US-11-045-024-7291  
Sequence 7291, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7291  
LENGTH: 9  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7291

Query Match 2.1%; Score 5; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194

DB 3 GATLE 7

RESULT 29

US-11-045-024-13707

Sequence 13707, Application US/11045024  
Publication No. US20050271676A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John

APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie

APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph

APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024

CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863

PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339

PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13707

LENGTH: 9

TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-13707

Query Match 2.1%; Score 5; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194

DB 4 GATLE 8

RESULT 30

US-10-431-638-29

Sequence 29, Application US/10431638  
Publication No. US2006003939A1

GENERAL INFORMATION:

APPLICANT: The Rockefeller Institute  
APPLICANT: Steller, Hermann

TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION  
FILE REFERENCE: P-5004-US

CURRENT APPLICATION NUMBER: US/10/431,638  
CURRENT FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 29  
LENGTH: 10

TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-431-638-29

Query Match 2.1%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSST 78

DB 3 RSSST 7

RESULT 31

US-11-045-024-1348

Sequence 1348, Application US/11045024  
Publication No. US20050271676A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John

APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie

APPLICANT: Celis, Esleben  
APPLICANT: Kubo, Ralph

APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024

CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863

PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339

PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610

;; PRIOR FILING DATE: 1994-12-01  
;; NUMBER OF SEQ ID NOS: 14528  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1348  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1348

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194  
DB 1 GATLE 5

## RESULT 32

US-11-045-024-5218  
;; Sequence 5218, Application US/11045024  
;; Publication No. US20050271676A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Livingston, Brian  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Baker, Denise Marie  
;; APPLICANT: Cello, Esteban  
;; APPLICANT: Kubo, Ralph  
;; APPLICANT: Grey, Howard M.  
;; APPLICANT: Eptimmune Inc.  
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
;; FILE REFERENCE: 2060.0040007  
;; CURRENT APPLICATION NUMBER: US/11/045,024  
;; CURRENT FILING DATE: 2005-01-28  
;; PRIOR APPLICATION NUMBER: US 09/412,863  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: US 08/027,146  
;; PRIOR FILING DATE: 1993-03-05  
;; PRIOR APPLICATION NUMBER: US 08/073,205  
;; PRIOR FILING DATE: 1993-06-04  
;; PRIOR APPLICATION NUMBER: US 08/103,396  
;; PRIOR FILING DATE: 1993-08-06  
;; PRIOR APPLICATION NUMBER: US 08/159,184  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/159,339  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/205,713  
;; PRIOR FILING DATE: 1994-03-04  
;; PRIOR APPLICATION NUMBER: US 08/347,610  
;; PRIOR FILING DATE: 1994-12-01  
;; NUMBER OF SEQ ID NOS: 14528  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5218  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5218

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194  
DB 3 GATLE 7

## RESULT 33

US-11-045-024-7293

;; Sequence 7293, Application US/11045024  
;; Publication No. US20050271676A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Livingston, Brian  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Baker, Denise Marie  
;; APPLICANT: Cello, Esteban  
;; APPLICANT: Kubo, Ralph  
;; APPLICANT: Grey, Howard M.  
;; APPLICANT: Eptimmune Inc.  
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
;; FILE REFERENCE: 2060.0040007  
;; CURRENT APPLICATION NUMBER: US/11/045,024  
;; CURRENT FILING DATE: 2005-01-28  
;; PRIOR APPLICATION NUMBER: US 09/412,863  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: US 08/027,146  
;; PRIOR FILING DATE: 1993-03-05  
;; PRIOR APPLICATION NUMBER: US 08/073,205  
;; PRIOR FILING DATE: 1993-06-04  
;; PRIOR APPLICATION NUMBER: US 08/103,396  
;; PRIOR FILING DATE: 1993-08-06  
;; PRIOR APPLICATION NUMBER: US 08/159,184  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/159,339  
;; PRIOR FILING DATE: 1993-11-29  
;; PRIOR APPLICATION NUMBER: US 08/205,713  
;; PRIOR FILING DATE: 1994-03-04  
;; PRIOR APPLICATION NUMBER: US 08/347,610  
;; PRIOR FILING DATE: 1994-12-01  
;; NUMBER OF SEQ ID NOS: 14528  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7293  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7293

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194  
DB 3 GATLE 7

RESULT 34  
US-11-045-024-9197  
;; Sequence 9197, Application US/11045024  
;; Publication No. US20050271676A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sette, Alessandro  
;; APPLICANT: Sidney, John  
;; APPLICANT: Southwood, Scott  
;; APPLICANT: Livingston, Brian  
;; APPLICANT: Chesnut, Robert  
;; APPLICANT: Baker, Denise Marie  
;; APPLICANT: Cello, Esteban  
;; APPLICANT: Kubo, Ralph  
;; APPLICANT: Grey, Howard M.  
;; APPLICANT: Eptimmune Inc.  
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
;; FILE REFERENCE: 2060.0040007  
;; CURRENT APPLICATION NUMBER: US/11/045,024  
;; CURRENT FILING DATE: 2005-01-28  
;; PRIOR APPLICATION NUMBER: US 09/412,863  
;; PRIOR FILING DATE: 1999-10-05

Query Match 2.1%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9197
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9197
```

```
Query Match          2.1%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          190 GATLE 194
DB          1 GATLE 5
```

```
RESULT 35
US-11-062-186-128
; Sequence 128, Application US/11062186
; Publication No. US20050272097A1
; GENERAL INFORMATION:
; APPLICANT: CALENOFF, EMANUEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; FILE REFERENCE: 21417-98470
; CURRENT APPLICATION NUMBER: US/11/062,186
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,062
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/545,980
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-062-186-128
```

```
Query Match          2.1%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          22 PASPL 26
DB          1 PASPL 5
```

```
RESULT 36
US-11-146-854-46
; Sequence 46, Application US/11146854
; Publication No. US20050277161A1
; GENERAL INFORMATION:
; APPLICANT: University of Virginia Patent Foundation
; APPLICANT: Engelhard, Victor H
; APPLICANT: Zarling, Angela
; APPLICANT: Hunt, Donald F
; APPLICANT: Evans, Anne M
```

```
; APPLICANT: Shabanowitz, Jeffrey
; TITLE OF INVENTION: PHOSPHOPEPTIDE ANTIGENS ASSOCIATED WITH MHC MOLECULES
; FILE REFERENCE: 01015-02
; CURRENT APPLICATION NUMBER: US/11/146,854
; PRIOR FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/578,205
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: PHOSPHORYLATION
US-11-146-854-46
```

```
Query Match          2.1%; Score 5; DB 7; Length 10;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          96 APRSP 100
DB          1 APRSP 5
```

```
RESULT 37
US-11-033-365-22
; Sequence 22, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Deerees, Shawn
; APPLICANT: Zogl, David
; APPLICANT: Wang, Zhiguang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-365-22
```

```
Query Match          2.1%; Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred.No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          20 LGPAS 24
DB          7 LGPAS 11
```

```
RESULT 38
US-11-058-735-69
; Sequence 69, Application US/11058735
; Publication No. US20050261475A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: TSENG, HUANG-CHUN
/ APPLICANT: TSAI, LI-HUEI
/ TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR
/ FILE REFERENCE: PHOSPHOPROTEOMIC ANALYSES
/ CURRENT APPLICATION NUMBER: US/11/058,735
/ CURRENT FILING DATE: 2005-02-14
/ PRIOR APPLICATION NUMBER: 60/544,748
/ PRIOR FILING DATE: 2004-02-13
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 69
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ US-11-058-735-69

Query Match      2.1% Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      80 SGGGD 84
      |||||
      5 SGGGD 9

Db

RESULT 39
US-11-119-098-67
/ Sequence 67, Application US/11119098
/ Publication No. US20050267030A1
/ GENERAL INFORMATION:
/ APPLICANT: Tsao, Philip S.
/ APPLICANT: Mochly-Rosen, Daria
/ TITLE OF INVENTION: Use of deltaPKC peptides for modulation of Reactive Oxygen Specie
/ FILE REFERENCE: 58600-8213, US00
/ CURRENT APPLICATION NUMBER: US/11/119,098
/ CURRENT FILING DATE: 2005-04-29
/ PRIOR APPLICATION NUMBER: US 60/567,315
/ PRIOR FILING DATE: 2004-04-30
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 67
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: modified delta VI-2 peptide
/ US-11-119-098-67

Query Match      2.1% Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      195 RPKTL 199
      |||||
      6 RPKTL 10

Db

RESULT 40
US-11-045-024-1456
/ Sequence 1456, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bastejan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ US-11-045-024-1456
```

```
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060,0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1456
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-1456

Query Match      2.1% Score 5; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      190 GATLE 194
      |||||
      5 GATLE 9

Db

RESULT 41
US-11-045-024-4215
/ Sequence 4215, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bastejan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060,0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1994-12-01
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
```

/ PRIOR APPLICATION NUMBER: US 08/347,610  
/ PRIOR FILING DATE: 1994-12-01  
/ NUMBER OF SEQ ID NOS: 14528  
/ SOFTWARE: FASTSEQ for Windows Version 4.0  
/ SEQ ID NO 4215  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-4215

Query Match 2.1%; Score 5; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194  
|||||  
DB 5 GATLE 9

RESULT 42  
US-11-045-024-7286  
/ Sequence 7286; Application US/11045024  
/ Publication No. US20050271676A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Livingston, Brian  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Baker, Denise Marie  
/ APPLICANT: Celis, Esceban  
/ APPLICANT: Kubo, Ralph  
/ APPLICANT: Grey, Howard M.  
/ APPLICANT: EpiImmune Inc.  
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0040007  
/ CURRENT APPLICATION NUMBER: US/11/045,024  
/ CURRENT FILING DATE: 2005-01-28  
/ PRIOR APPLICATION NUMBER: US 09/412,863  
/ PRIOR FILING DATE: 1999-10-05  
/ PRIOR APPLICATION NUMBER: US 08/027,146  
/ PRIOR FILING DATE: 1993-03-05  
/ PRIOR APPLICATION NUMBER: US 08/073,205  
/ PRIOR FILING DATE: 1993-06-04  
/ PRIOR APPLICATION NUMBER: US 08/103,396  
/ PRIOR FILING DATE: 1993-08-06  
/ PRIOR APPLICATION NUMBER: US 08/159,184  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/159,339  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/205,713  
/ PRIOR FILING DATE: 1994-03-04  
/ PRIOR APPLICATION NUMBER: US 08/347,610  
/ PRIOR FILING DATE: 1994-12-01  
/ NUMBER OF SEQ ID NOS: 14528  
/ SOFTWARE: FASTSEQ for Windows Version 4.0  
/ SEQ ID NO 7286  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7286

Query Match 2.1%; Score 5; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194  
|||||  
DB 5 GATLE 9

RESULT 43

US-11-045-024-9071  
/ Sequence 9071; Application US/11045024  
/ Publication No. US20050271676A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Livingston, Brian  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Baker, Denise Marie  
/ APPLICANT: Celis, Esceban  
/ APPLICANT: Kubo, Ralph  
/ APPLICANT: Grey, Howard M.  
/ APPLICANT: EpiImmune Inc.  
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0040007  
/ CURRENT APPLICATION NUMBER: US/11/045,024  
/ CURRENT FILING DATE: 2005-01-28  
/ PRIOR APPLICATION NUMBER: US 09/412,863  
/ PRIOR FILING DATE: 1999-10-05  
/ PRIOR APPLICATION NUMBER: US 08/027,146  
/ PRIOR FILING DATE: 1993-03-05  
/ PRIOR APPLICATION NUMBER: US 08/073,205  
/ PRIOR FILING DATE: 1993-06-04  
/ PRIOR APPLICATION NUMBER: US 08/103,396  
/ PRIOR FILING DATE: 1993-08-06  
/ PRIOR APPLICATION NUMBER: US 08/159,184  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/159,339  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/205,713  
/ PRIOR FILING DATE: 1994-03-04  
/ PRIOR APPLICATION NUMBER: US 08/347,610  
/ PRIOR FILING DATE: 1994-12-01  
/ NUMBER OF SEQ ID NOS: 14528  
/ SOFTWARE: FASTSEQ for Windows Version 4.0  
/ SEQ ID NO 9071  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-9071

Query Match 2.1%; Score 5; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 GATLE 194  
|||||  
DB 2 GATLE 6

RESULT 44  
US-10-986-501-220  
/ Sequence 220; Application US/10986501  
/ Publication No. US2005024845A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: 90 Human Secreted Proteins  
/ FILE REFERENCE: P2013P2C1  
/ CURRENT APPLICATION NUMBER: US/10/986,501  
/ CURRENT FILING DATE: 2004-11-12  
/ PRIOR APPLICATION NUMBER: US/10/621,363  
/ PRIOR FILING DATE: 2003-07-18  
/ PRIOR APPLICATION NUMBER: 09/969,730  
/ PRIOR FILING DATE: 2001-10-06  
/ PRIOR APPLICATION NUMBER: 09/774,639  
/ PRIOR FILING DATE: 2001-02-01  
/ PRIOR APPLICATION NUMBER: 60/238,291  
/ PRIOR FILING DATE: 2000-10-06  
/ PRIOR APPLICATION NUMBER: 09/244,112  
/ PRIOR FILING DATE: 1999-02-04  
/ PRIOR APPLICATION NUMBER: PCT/US98/16235

```

; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-220
```

```

Query Match
Best Local Similarity 2.1%; Score 5; DB 6; Length 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 24 SPLDS 28
Db 2 SPLDS 6
```

```

RESULT 45
US-11-054-515-2364
; Sequence 2364, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2364
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2364
```

```

Query Match
Best Local Similarity 2.1%; Score 5; DB 7; Length 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 22 PASPL 26
Db 8 PASPL 12
```

```

RESULT 46
US-11-054-515-2390
; Sequence 2390, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2390
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2390
```

```

Query Match
Best Local Similarity 2.1%; Score 5; DB 7; Length 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 22 PASPL 26
Db 8 PASPL 12
```

```

RESULT 47
US-11-054-515-2417
; Sequence 2417, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2417
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2417

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; Publication No. US20050255532A1
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
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; PRIOR FILING DATE: 2001-11-16
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
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US-11-054-515-2420

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; GENERAL INFORMATION:
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
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; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
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; PRIOR APPLICATION NUMBER: 60/580,347
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US-11-054-515-2445

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; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR FILING DATE: 2000-10-17
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Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 3247  
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 US-11-054-515-2464

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Qy 99 SPLAP 103  
 Db 10 SPLAP 14

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 Job time : 32 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: January 18, 2006, 21:06:40 ; Search time 30 Seconds  
(without alignments)  
3.378 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 70606 seqs, 10133861 residues

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Total number of hits satisfying chosen parameters: 21200

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 200 summaries

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Published Applications AA New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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; Sequence 607, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REF-2010US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 607
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-607

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Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
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Db       1 EYLVPOQGF 9

RESULT 2
US-11-110-274-308
; Sequence 308, Application US/11110274
; Publication No. US20050266502A1
; GENERAL INFORMATION:
```

APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting  
FILE REFERENCE: P27,697-A USA  
CURRENT APPLICATION NUMBER: US/11/110,274  
PRIOR FILING DATE: 2005-04-20  
PRIOR APPLICATION NUMBER: US 60/563,661  
NUMBER OF SEQ ID NOS: 620  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 308  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-110-274-308

Query Match 40.0%; Score 4; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVP 6  
DB 1 YLVP 4

RESULT 3  
US-11-057-708-24  
Sequence 24, Application US/11057708  
Publication No. US20050250702A1  
GENERAL INFORMATION:  
APPLICANT: Universiteit Utrecht  
APPLICANT: Strous, Gerardus  
APPLICANT: Van Kerkhof, Petrus  
APPLICANT: Govers, Roland  
TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEIN  
TITLE OF INVENTION: INHIBITORS OR RECEPTOR FRAGMENTS  
FILE REFERENCE: 2183-4525US  
CURRENT APPLICATION NUMBER: US/11/057,708  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: US/09/660,302  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: PCT/NL99/00136  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: EP98200799.9  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 24  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Rattus unknown species (Rat)  
FEATURE:  
OTHER INFORMATION: MHC-II(BETA)  
US-11-057-708-24

Query Match 40.0%; Score 4; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYL 4  
DB 3 EBYL 6

RESULT 4  
US-11-057-708-32  
Sequence 32, Application US/11057708  
Publication No. US20050250702A1  
GENERAL INFORMATION:  
APPLICANT: Universiteit Utrecht  
APPLICANT: Strous, Gerardus

APPLICANT: Van Kerkhof, Petrus  
APPLICANT: Govers, Roland  
TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEIN  
TITLE OF INVENTION: INHIBITORS OR RECEPTOR FRAGMENTS  
FILE REFERENCE: 2183-4525US  
CURRENT APPLICATION NUMBER: US/11/057,708  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: US/09/660,302  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: PCT/NL99/00136  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: EP98200799.9  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Unnaure, RHESUS BLOOD GROUP-ASSOCIATED GLYCOPROTEIN  
US-11-057-708-32

Query Match 40.0%; Score 4; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLV 5  
DB 4 EYLV 7

RESULT 5  
US-10-997-066-17  
Sequence 17, Application US/10997066  
Publication No. US20050244891A1  
GENERAL INFORMATION:  
APPLICANT: GRAHAM, RONALD J.  
APPLICANT: LEE, LINDA G.  
APPLICANT: SUN, HONGYE  
TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF  
FILE REFERENCE: 375461-0110US  
CURRENT APPLICATION NUMBER: US/10/997,066  
CURRENT FILING DATE: 2004-11-24  
PRIOR APPLICATION NUMBER: 60/525,492  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/628,509  
PRIOR FILING DATE: 2004-11-15  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 17  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-997-066-17

Query Match 30.0%; Score 3; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBY 3  
DB 2 EBY 4

RESULT 6  
US-11-035-682-13  
Sequence 13, Application US/11035682  
Publication No. US20050245726A1  
GENERAL INFORMATION:

APPLICANT: LEE, LINDA G.  
APPLICANT: SUN, HONGYE  
TITLE OF INVENTION: FLUOROGENIC KINASE ASSAYS AND SUBSTRATES  
FILE REFERENCE: 375461-023US  
CURRENT APPLICATION NUMBER: US/11/035,682  
CURRENT FILING DATE: 2005-01-14  
PRIOR APPLICATION NUMBER: 60/537,416  
PRIOR FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 13  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-035-682-13

Query Match 30.0%; Score 3; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEY 3  
|||  
Db 2 BEY 4

RESULT 7  
US-10-969-314-36  
Sequence 36, Application US/10969314  
Publication No. US20050249719A1  
GENERAL INFORMATION:  
APPLICANT: SHAN, LI  
APPLICANT: BETHUNE, MICHAEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: GASS, JONATHAN  
APPLICANT: PYLE, GAIL G.  
APPLICANT: GRAY, GARY  
APPLICANT: ISAACS, INDU  
APPLICANT: STROHMEIER, GREGG  
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR  
FILE REFERENCE: STAN-361  
CURRENT APPLICATION NUMBER: US/10/969,314  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: 60/565,668  
PRIOR FILING DATE: 2004-04-26  
PRIOR APPLICATION NUMBER: 10/367,405  
PRIOR FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: 60/357,238  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: 60/380,761  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: 60/392,782  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/422,933  
PRIOR FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 36  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Triticum aestivum  
US-10-969-314-36

Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQO 8  
|||  
Db 2 PQO 4

RESULT 8  
US-10-485-788A-458  
Sequence 458, Application US/10485788A  
Publication No. US20050282743A1  
GENERAL INFORMATION:  
APPLICANT: Lu, Peter S.  
APPLICANT: Rabinowitz, Joshua D.  
APPLICANT: Schmelzer, Johannes  
APPLICANT: Carrick, Deanna Marie  
APPLICANT: Arbor Vita Corporation  
TITLE OF INVENTION: Molecular Interactions in Cells  
FILE REFERENCE: 20054-00320US  
CURRENT APPLICATION NUMBER: US/10/485,788A  
CURRENT FILING DATE: 2004-02-03  
PRIOR APPLICATION NUMBER: US 60/309,841  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/360,061  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
PRIOR FILING DATE: 2002-08-02  
NUMBER OF SEQ ID NOS: 841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 458  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-485-788A-458

Query Match 30.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
|||  
Db 1 YLV 3

RESULT 9  
US-11-014-629-4  
Sequence 4, Application US/11014629  
Publication No. US20050244376A1  
GENERAL INFORMATION:  
APPLICANT: Hall, Frederick L.  
APPLICANT: Gordon, Erlinda M.  
TITLE OF INVENTION: TARGETED GENE DELIVERY TO EXTRACELLULAR MATRIX  
FILE REFERENCE: 30863-704.302  
CURRENT APPLICATION NUMBER: US/11/014,629  
CURRENT FILING DATE: 2004-12-15  
PRIOR APPLICATION NUMBER: US 08/837,223  
PRIOR FILING DATE: 1997-04-10  
PRIOR APPLICATION NUMBER: US 09/904,923  
PRIOR FILING DATE: 2001-07-13  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide cleavage site  
US-11-014-629-4

Query Match 30.0%; Score 3; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 1 LVP 3

```
RESULT 10
US-11-148-074-8
; Sequence 8, Application US/11148074
; Publication No. US20050272919A1
; GENERAL INFORMATION:
; APPLICANT: Duellman, Sarah
; APPLICANT: Thompson, Nancy
; APPLICANT: Burgess, Richard
; TITLE OF INVENTION: Immunodiffusible Chromatography Using Epitope Tags to
; FILE REFERENCE: 09820.315
; CURRENT APPLICATION NUMBER: US/11148,074
; PRIOR FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: US 60/577,944
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Thrombin protease recognition sequence
US-11-148-074-8

Query Match          30.0%; Score 3; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6
DB 1 LVP 3

RESULT 11
US-11-107-539-2
; Sequence 2, Application US/11107539
; Publication No. US20060002917A1
; GENERAL INFORMATION:
; APPLICANT: PIPER, JUSTIN L.
; APPLICANT: GRAY, GARY M.
; APPLICANT: KHOSLA, CHAITAN
; TITLE OF INVENTION: EFFECT OF PROLYL ENDOPEPTIDASE ON
; FILE REFERENCE: STAN-362
; CURRENT APPLICATION NUMBER: US/11/107,539
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/565,684
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Trilicium aestivum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Tyrosine modified with NO2
US-11-107-539-2

Query Match          30.0%; Score 3; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 POO 8
DB 2 POO 4

RESULT 12
US-10-467-657-9179
; Sequence 9179, Application US/10467657
```

```
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9179
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9179

Query Match          30.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5
DB 3 YLV 5

RESULT 13
US-10-485-788A-459
; Sequence 459, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 459
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-459

Query Match          30.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5
DB 2 YLV 4

RESULT 14
US-10-880-238-133
; Sequence 133, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Wing-Tai
```

```
/ APPLICANT: Cheng, Man
/ TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
/ TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING
/ FILE REFERENCE: 17329-003001
/ CURRENT APPLICATION NUMBER: US/10/880,238
/ CURRENT FILING DATE: 2004-06-29
/ NUMBER OF SEQ ID NOS: 214
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 133
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-133
```

```
Query Match      30.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 YLV 5
        |||
Db      2 YLV 4
```

```
RESULT 15
US-11-201-341-14
/ Sequence 14, Application US/11201341
/ Publication No. US20050287564A1
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Gilbertson, Debra G.
/ TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
/ FILE REFERENCE: 97-38C2
/ CURRENT APPLICATION NUMBER: US/11/201,341
/ CURRENT FILING DATE: 2005-08-10
/ PRIOR APPLICATION NUMBER: US 10/010,050
/ PRIOR FILING DATE: 2001-11-09
/ PRIOR APPLICATION NUMBER: US 09/122,383
/ PRIOR FILING DATE: 1998-07-24
/ PRIOR APPLICATION NUMBER: US 60/053,613
/ PRIOR FILING DATE: 1997-07-24
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Glu-Glu affinity tag peptide
US-11-201-341-14
```

```
Query Match      30.0%; Score 3; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EEY 3
        |||
Db      1 EEY 3
```

```
RESULT 16
US-11-150-533-53
/ Sequence 53, Application US/11150533
/ Publication No. US2006002925A1
/ GENERAL INFORMATION:
/ APPLICANT: Presnell, Scott R.
/ APPLICANT: Burkhead, Steven K.
/ APPLICANT: Levin, Steven D.
/ APPLICANT: Kuestner, Rolf E.
/ APPLICANT: Gao, Zeren
/ APPLICANT: Jaspers, Stephen R.
```

```
/ APPLICANT: Bilsborough, Janine
/ TITLE OF INVENTION: SOLUBLE ZCYTOR14, ANTI-ZCYTOR14
/ TITLE OF INVENTION: ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING IN
/ TITLE OF INVENTION: INFLAMMATION
/ FILE REFERENCE: 04-06P1
/ CURRENT APPLICATION NUMBER: US/11/150,533
/ CURRENT FILING DATE: 2005-06-10
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 53
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Glu-Glu tag
US-11-150-533-53
```

```
Query Match      30.0%; Score 3; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EEY 3
        |||
Db      1 EEY 3
```

```
RESULT 17
US-10-485-788A-370
/ Sequence 370, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Schweitzer, Johannes
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Arbor Vita Corporation
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-003320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ CURRENT FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 370
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-485-788A-370
```

```
Query Match      30.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 PQQ 8
        |||
Db      2 PQQ 4
```

```
RESULT 18
US-10-485-788A-460
/ Sequence 460, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Schweitzer, Johannes
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Arbor Vita Corporation
```



/ TITLE OF INVENTION: Molecular Interactions in Cells  
/ FILE REFERENCE: 20054-003320US  
/ CURRENT APPLICATION NUMBER: US/10/485,788A  
/ CURRENT FILING DATE: 2004-02-03  
/ PRIOR APPLICATION NUMBER: US 60/309,841  
/ PRIOR FILING DATE: 2001-08-03  
/ PRIOR APPLICATION NUMBER: US 60/360,061  
/ PRIOR FILING DATE: 2002-02-25  
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
/ PRIOR FILING DATE: 2002-08-02  
/ NUMBER OF SEQ ID NOS: 841  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO: 460  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-485-788A-460

Query Match 30.0%; Score 3; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 3 YLV 5

RESULT 19  
US-11-044-051-91  
/ Sequence 91, Application US/11044051  
/ Publication No. US2005025553A1  
/ GENERAL INFORMATION:  
/ APPLICANT: VAN PEL, Aline  
/ APPLICANT: GODELAINE, Daniel  
/ APPLICANT: CARRASCO, Javier  
/ APPLICANT: BRASSEUR, Francis  
/ APPLICANT: BOON-FALEUR, Thierry  
/ TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF  
/ FILE REFERENCE: LUD 5888 US  
/ CURRENT APPLICATION NUMBER: US/11/044,051  
/ CURRENT FILING DATE: 2005-01-28  
/ PRIOR APPLICATION NUMBER: US 60/459,263  
/ PRIOR FILING DATE: 2004-02-09  
/ NUMBER OF SEQ ID NOS: 111  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO: 91  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-044-051-91

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 5 YLV 7

RESULT 20  
US-11-044-051-92  
/ Sequence 92, Application US/11044051  
/ Publication No. US2005025553A1  
/ GENERAL INFORMATION:  
/ APPLICANT: VAN PEL, Aline  
/ APPLICANT: GODELAINE, Daniel  
/ APPLICANT: CARRASCO, Javier  
/ APPLICANT: BRASSEUR, Francis  
/ APPLICANT: BOON-FALEUR, Thierry  
/ TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF  
/ FILE REFERENCE: LUD 5888 US  
/ CURRENT APPLICATION NUMBER: US/11/044,051

/ CURRENT FILING DATE: 2005-01-28  
/ PRIOR APPLICATION NUMBER: US 60/459,263  
/ PRIOR FILING DATE: 2004-02-09  
/ NUMBER OF SEQ ID NOS: 111  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO: 92  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-044-051-92

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 6 YLV 8

RESULT 21  
US-11-045-024-189  
/ Sequence 189, Application US/11045024  
/ Publication No. US20050271676A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Livingston, Brian  
/ APPLICANT: Chennut, Robert  
/ APPLICANT: Baker, Denise Marie  
/ APPLICANT: Celis, Etseban  
/ APPLICANT: Kubo, Ralph  
/ APPLICANT: Grey, Howard M.  
/ APPLICANT: Epimmune Inc.  
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
/ FILE REFERENCE: 2060.0040007  
/ CURRENT APPLICATION NUMBER: US/11/045,024  
/ CURRENT FILING DATE: 2005-01-28  
/ PRIOR APPLICATION NUMBER: US 09/412,863  
/ PRIOR FILING DATE: 1999-10-05  
/ PRIOR APPLICATION NUMBER: US 08/027,146  
/ PRIOR FILING DATE: 1993-03-05  
/ PRIOR APPLICATION NUMBER: US 08/073,205  
/ PRIOR FILING DATE: 1993-06-04  
/ PRIOR APPLICATION NUMBER: US 08/103,396  
/ PRIOR FILING DATE: 1993-08-06  
/ PRIOR APPLICATION NUMBER: US 08/159,184  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/159,339  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/205,713  
/ PRIOR FILING DATE: 1994-03-04  
/ PRIOR APPLICATION NUMBER: US 08/347,610  
/ PRIOR FILING DATE: 1994-12-01  
/ NUMBER OF SEQ ID NOS: 14528  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO: 189  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-189

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QGF 10  
DB 6 QGF 8

```
RESULT 22
US-11-045-024-1573
; Sequence 1573, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1573
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1573

Query Match      30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 QQG 9
      |||
Db      4 QQG 6

RESULT 23
US-11-045-024-3090
; Sequence 3090, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
```

```
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3090
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3090

Query Match      30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LVP 6
      |||
Db      2 LVP 4

RESULT 24
US-11-045-024-4235
; Sequence 4235, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4235
; LENGTH: 8
```

```

; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4235
Query Match          30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 QGF 10
      |||
      5 QGF 7

Db

RESULT 25
US-11-045-024-4237
; Sequence 4237, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4237
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4237
Query Match          30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 QGF 10
      |||
      5 QGF 7

Db

RESULT 26
US-11-045-024-5505
; Sequence 5505, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
```

```

; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5505
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5505
Query Match          30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 QGF 10
      |||
      6 QGF 8

Db

RESULT 27
US-11-045-024-7435
; Sequence 7435, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
```

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; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7435
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7435

Query Match      30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 QGF 10
Db      6 QGF 8

RESULT 28
US-11-045-024-7461
; Sequence 7461, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7461
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7461

Query Match      30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      8 QGF 10
Db      2 QGF 4

RESULT 29
US-11-045-024-9375
; Sequence 9375, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9375
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9375

Query Match      30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LVP 6
Db      2 LVP 4

RESULT 30
US-11-045-024-9399
; Sequence 9399, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
```

APPLICANT: BpImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
VIRUS-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
PRIORITY FILING DATE: 2005-01-28  
PRIORITY APPLICATION NUMBER: US 09/412,863  
PRIORITY FILING DATE: 1999-10-05  
PRIORITY APPLICATION NUMBER: US 08/027,146  
PRIORITY FILING DATE: 1993-03-05  
PRIORITY APPLICATION NUMBER: US 08/073,205  
PRIORITY FILING DATE: 1993-06-04  
PRIORITY APPLICATION NUMBER: US 08/103,396  
PRIORITY FILING DATE: 1993-08-06  
PRIORITY APPLICATION NUMBER: US 08/159,184  
PRIORITY FILING DATE: 1993-11-29  
PRIORITY APPLICATION NUMBER: US 08/159,339  
PRIORITY FILING DATE: 1993-11-29  
PRIORITY APPLICATION NUMBER: US 08/205,713  
PRIORITY FILING DATE: 1994-03-04  
PRIORITY APPLICATION NUMBER: US 08/347,610  
PRIORITY FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9399  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-9399

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QCG 10  
|||  
Db 6 QCG 8

RESULT 31  
US-11-045-024-9713  
Sequence 9713, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Betteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: BpImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
VIRUS-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
PRIORITY FILING DATE: 2005-01-28  
PRIORITY APPLICATION NUMBER: US 09/412,863  
PRIORITY FILING DATE: 1999-10-05  
PRIORITY APPLICATION NUMBER: US 08/027,146  
PRIORITY FILING DATE: 1993-03-05  
PRIORITY APPLICATION NUMBER: US 08/073,205  
PRIORITY FILING DATE: 1993-06-04  
PRIORITY APPLICATION NUMBER: US 08/103,396  
PRIORITY FILING DATE: 1993-08-06  
PRIORITY APPLICATION NUMBER: US 08/159,184  
PRIORITY FILING DATE: 1993-11-29  
PRIORITY APPLICATION NUMBER: US 08/159,339  
PRIORITY FILING DATE: 1993-11-29  
PRIORITY APPLICATION NUMBER: US 08/205,713  
PRIORITY FILING DATE: 1994-03-04

PRIORITY APPLICATION NUMBER: US 08/347,610  
PRIORITY FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9713  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-9713

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QCG 9  
|||  
Db 4 QCG 6

RESULT 32  
US-11-045-024-9714  
Sequence 9714, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Betteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: BpImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
VIRUS-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
PRIORITY FILING DATE: 2005-01-28  
PRIORITY APPLICATION NUMBER: US 09/412,863  
PRIORITY FILING DATE: 1999-10-05  
PRIORITY APPLICATION NUMBER: US 08/027,146  
PRIORITY FILING DATE: 1993-03-05  
PRIORITY APPLICATION NUMBER: US 08/073,205  
PRIORITY FILING DATE: 1993-06-04  
PRIORITY APPLICATION NUMBER: US 08/103,396  
PRIORITY FILING DATE: 1993-08-06  
PRIORITY APPLICATION NUMBER: US 08/159,184  
PRIORITY FILING DATE: 1993-11-29  
PRIORITY APPLICATION NUMBER: US 08/159,339  
PRIORITY FILING DATE: 1993-11-29  
PRIORITY APPLICATION NUMBER: US 08/205,713  
PRIORITY FILING DATE: 1994-03-04  
PRIORITY APPLICATION NUMBER: US 08/347,610  
PRIORITY FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9714  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-9714

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QCG 9  
|||  
Db 3 QCG 5

RESULT 33

```
US-11-045-024-11467
; Sequence 11467, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11467
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-11467

Query Match          30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 LVP 6
        |||
Db      2 LVP 4

RESULT 34
US-11-045-024-11705
; Sequence 11705, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
```

```
US-11-045-024-11705
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11705
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-11705

Query Match          30.0%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 OOG 9
        |||
Db      3 OOG 5

RESULT 35
US-11-045-024-12655
; Sequence 12655, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12655
; LENGTH: 8
; TYPE: PRT
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ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-12655

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QCF 10  
DB 5 QCF 7

RESULT 36  
US-11-041-270A-9

Sequence 9, Application US/11041270A  
Publication No. US20050276854A1  
GENERAL INFORMATION:  
APPLICANT: TRIGG, TIMOTHY ELLIOT  
APPLICANT: WALSH, JOHN DESMOND  
APPLICANT: RATHJEN, DEBORAH ANN  
TITLE OF INVENTION: BIOTRIMPLANT FORMULATION  
FILE REFERENCE: 4137-43  
CURRENT APPLICATION NUMBER: US/11/041,270A  
CURRENT FILING DATE: 2005-01-25  
PRIOR APPLICATION NUMBER: PCT/AU99/00585  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: AU PP 4730  
PRIOR FILING DATE: 1998-07-20  
PRIOR APPLICATION NUMBER: AU PP 4731  
PRIOR FILING DATE: 1998-07-20  
PRIOR APPLICATION NUMBER: AU PP 0324  
PRIOR FILING DATE: 1999-05-13  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: substance P antagonist  
OTHER INFORMATION: C-term amidated  
US-11-041-270A-9

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PQQ 8  
DB 1 PQQ 3

RESULT 37  
US-11-064-416-4

Sequence 4, Application US/11064416  
Publication No. US20060008461A1  
GENERAL INFORMATION:  
APPLICANT: Oregon Health & Science University  
APPLICANT: Vatvlin, Milton B  
APPLICANT: Stowell, Michael HB  
APPLICANT: Gillicchio, Vincent S  
APPLICANT: Meredith, Michael J  
TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING  
FILE REFERENCE: 899-71532  
CURRENT APPLICATION NUMBER: US/11/064,416  
CURRENT FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: 10/050,271  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 09/573,497  
PRIOR FILING DATE: 2000-05-16  
PRIOR APPLICATION NUMBER: 09/060,011

PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 08/691,891  
PRIOR FILING DATE: 1996-08-01  
PRIOR APPLICATION NUMBER: 08/441,770  
PRIOR FILING DATE: 1995-05-16  
PRIOR APPLICATION NUMBER: 08/246,941  
PRIOR FILING DATE: 1994-05-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 4  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: peptide linker  
US-11-064-416-4

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 5 YLV 7

RESULT 38  
US-11-064-416-5

Sequence 5, Application US/11064416  
Publication No. US20060008461A1  
GENERAL INFORMATION:  
APPLICANT: Oregon Health & Science University  
APPLICANT: Vatvlin, Milton B  
APPLICANT: Stowell, Michael HB  
APPLICANT: Gillicchio, Vincent S  
APPLICANT: Meredith, Michael J  
TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING  
FILE REFERENCE: 899-71532  
CURRENT APPLICATION NUMBER: US/11/064,416  
CURRENT FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: 10/050,271  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 09/573,497  
PRIOR FILING DATE: 2000-05-16  
PRIOR APPLICATION NUMBER: 09/060,011  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 08/691,891  
PRIOR FILING DATE: 1996-08-01  
PRIOR APPLICATION NUMBER: 08/441,770  
PRIOR FILING DATE: 1995-05-16  
PRIOR APPLICATION NUMBER: 08/246,941  
PRIOR FILING DATE: 1994-05-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: peptide linker  
US-11-064-416-5

Query Match 30.0%; Score 3; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLV 5  
DB 4 YLV 6

RESULT 39  
US-10-969-314-30

```
/ Sequence 30, Application US/10969314
/ Publication No. US20050249719A1
/ GENERAL INFORMATION:
/ APPLICANT: SHAN, LU
/ APPLICANT: BETHUNE, MICHAEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: GASS, JONATHAN
/ APPLICANT: PYLE, GAIL G.
/ APPLICANT: GRAY, GARY
/ APPLICANT: ISAACS, INDU
/ APPLICANT: STROHMEIER, GREGG
/ TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
/ FILE REFERENCE: STAN-361
/ CURRENT APPLICATION NUMBER: US/10/969,314
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: 60/565,668
/ PRIOR FILING DATE: 2004-04-26
/ PRIOR APPLICATION NUMBER: 10/367,405
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/357,238
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: 60/380,761
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 60/392,782
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-969-314-30

Query Match      30.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PQQ 8
      |||
Db      3 PQQ 5

RESULT 40
US-10-969-314-31
/ Sequence 31, Application US/10969314
/ Publication No. US20050249719A1
/ GENERAL INFORMATION:
/ APPLICANT: SHAN, LU
/ APPLICANT: BETHUNE, MICHAEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: GASS, JONATHAN
/ APPLICANT: PYLE, GAIL G.
/ APPLICANT: GRAY, GARY
/ APPLICANT: ISAACS, INDU
/ APPLICANT: STROHMEIER, GREGG
/ TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
/ FILE REFERENCE: STAN-361
/ CURRENT APPLICATION NUMBER: US/10/969,314
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: 60/565,668
/ PRIOR FILING DATE: 2004-04-26
/ PRIOR APPLICATION NUMBER: 10/367,405
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/357,238
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: 60/380,761
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 60/392,782
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-969-314-32
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/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 31
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-969-314-31

Query Match      30.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PQQ 8
      |||
Db      3 PQQ 5

RESULT 41
US-10-969-314-32
/ Sequence 32, Application US/10969314
/ Publication No. US20050249719A1
/ GENERAL INFORMATION:
/ APPLICANT: SHAN, LU
/ APPLICANT: BETHUNE, MICHAEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: GASS, JONATHAN
/ APPLICANT: PYLE, GAIL G.
/ APPLICANT: GRAY, GARY
/ APPLICANT: ISAACS, INDU
/ APPLICANT: STROHMEIER, GREGG
/ TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
/ FILE REFERENCE: STAN-361
/ CURRENT APPLICATION NUMBER: US/10/969,314
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: 60/565,668
/ PRIOR FILING DATE: 2004-04-26
/ PRIOR APPLICATION NUMBER: 10/367,405
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/357,238
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: 60/380,761
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 60/392,782
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-969-314-32

Query Match      30.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PQQ 8
      |||
Db      3 PQQ 5

RESULT 42
US-10-969-314-33
/ Sequence 33, Application US/10969314
/ Publication No. US20050249719A1
/ GENERAL INFORMATION:
/ APPLICANT: SHAN, LU
/ APPLICANT: BETHUNE, MICHAEL
```



APPLICANT: KHOSIA, CHAITAN  
APPLICANT: GASS, JONATHAN  
APPLICANT: FYLE, GARY G.  
APPLICANT: GRAY, GARY  
APPLICANT: ISAACS, INDU  
APPLICANT: STROHMEIER, GREGG  
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR  
FILE REFERENCE: STAN-361  
CURRENT APPLICATION NUMBER: US/10/969,314  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: 60/565,668  
PRIOR FILING DATE: 2004-04-26  
PRIOR APPLICATION NUMBER: 10/367,405  
PRIOR FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: 60/357,238  
PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: 60/380,761  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: 60/392,782  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/422,933  
PRIOR FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Trifolium aestivum  
US-10-969-314-33

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PQQ 8  
Db 5 PQQ 7

RESULT 43  
US-10-925-366A-33  
Sequence 33, Application US/10925366A  
Publication No. US20050271663A1  
GENERAL INFORMATION:  
APPLICANT: Ignatovich, Olga  
APPLICANT: Demildt, Rudolph M.T.  
APPLICANT: Benjamin, Woolven  
APPLICANT: Grant, Steven  
APPLICANT: Jones, Philip  
APPLICANT: Bastran, Amrik  
APPLICANT: Brewis, Neil  
TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders  
FILE REFERENCE: 8039/2105  
CURRENT APPLICATION NUMBER: US/10/925,366A  
CURRENT FILING DATE: 2004-08-24  
PRIOR APPLICATION NUMBER: US 10/744,774  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: PCT/GB2003/002804  
PRIOR FILING DATE: 2003-06-30  
PRIOR APPLICATION NUMBER: PCT/GB2002/03014  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: GB 0230202.4  
PRIOR FILING DATE: 2002-12-27  
PRIOR APPLICATION NUMBER: GB 115841.9  
PRIOR FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: PCT/GB2004/002829  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: US 60/535,076  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: PCT/GB2003/005646  
PRIOR FILING DATE: 2003-12-24  
PRIOR APPLICATION NUMBER: GB 0327706.8

PRIOR FILING DATE: 2003-11-28  
PRIOR APPLICATION NUMBER: US 60/509,613  
PRIOR FILING DATE: 2003-10-08  
NUMBER OF SEQ ID NOS: 368  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 33  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial CDR3 Sequence  
US-10-925-366A-33

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PQQ 9  
Db 1 PQQ 3

RESULT 44  
US-10-925-366A-72  
Sequence 72, Application US/10925366A  
Publication No. US20050271663A1  
GENERAL INFORMATION:  
APPLICANT: Ignatovich, Olga  
APPLICANT: Demildt, Rudolph M.T.  
APPLICANT: Benjamin, Woolven  
APPLICANT: Grant, Steven  
APPLICANT: Jones, Philip  
APPLICANT: Bastran, Amrik  
APPLICANT: Brewis, Neil  
TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders  
FILE REFERENCE: 8039/2105  
CURRENT APPLICATION NUMBER: US/10/925,366A  
CURRENT FILING DATE: 2004-08-24  
PRIOR APPLICATION NUMBER: US 10/744,774  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: PCT/GB2003/002804  
PRIOR FILING DATE: 2003-06-30  
PRIOR APPLICATION NUMBER: PCT/GB2002/03014  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: GB 0230202.4  
PRIOR FILING DATE: 2002-12-27  
PRIOR APPLICATION NUMBER: GB 115841.9  
PRIOR FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: PCT/GB2004/002829  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: US 60/535,076  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: PCT/GB2003/005646  
PRIOR FILING DATE: 2003-12-24  
PRIOR APPLICATION NUMBER: GB 0327706.8  
PRIOR FILING DATE: 2003-11-28  
PRIOR APPLICATION NUMBER: US 60/509,613  
PRIOR FILING DATE: 2003-10-08  
NUMBER OF SEQ ID NOS: 368  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 72  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial CDR3 Sequence  
US-10-925-366A-72

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PQQ 9

Db 1 OOG 3

## RESULT 45

US-10-966-483-8  
; Sequence 8, Application US/10966483  
; Publication No. US20050281783A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael S.  
; APPLICANT: Kienner, Peter A.  
; APPLICANT: Bruckheimer, Elizabeth  
; APPLICANT: Dubensky, Jr. Thomas W.  
; APPLICANT: Cook, David N.  
; TITLE OF INVENTION: LISTERIA-BASED BphA2 VACCINES  
; FILE REFERENCE: 10271-146  
; CURRENT APPLICATION NUMBER: US/10/966,483  
; PRIOR FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: US 60/511,919  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: US 60/511,719  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: US 60/532,666  
; PRIOR FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/556,631  
; PRIOR FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2004-10-07  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-966-483-8

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 2 LVP 4

## RESULT 46

US-10-859-643-19  
; Sequence 19, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161p2f10b Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-19

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 5 LVP 7

## RESULT 47

US-10-859-643-32  
; Sequence 32, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161p2f10b Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-32

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVP 6  
|||  
Db 2 LVP 4

## RESULT 48

US-10-859-643-271  
; Sequence 271, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161p2f10b Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 271  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-271

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LVP 6  
|||  
Db 1 LVP 3

## RESULT 49

US-10-859-643-352  
; Sequence 352, Application US/10859643  
; Publication No. US2006002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 352  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-352

Query Match 30.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYL 4  
|||  
Db 1 EYL 3

## RESULT 50

US-10-859-643-487  
; Sequence 487, Application US/10859643  
; Publication No. US2006002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 487  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-487

Query Match 30.0%; Score 3; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPO 7  
|||  
Db 6 VPO 8

Search completed: January 18, 2006, 21:17:47  
Job time : 32 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 20:45:40 ; Search time 72 Seconds  
(without alignments)  
2302.766 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EFSRMRAPQRFVVIQNE...AVENPEVILPQGAAPQHP 235

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1027535

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database: UniProt 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.4	95	1 ERBB4_MOUSE	061527 mus musculu
2	8	3.4	145	2 OBRP3_STRAW	082E38 streptomyce
3	8	3.4	160	2 O68A27_RHOSH	068A27 rhodobacter
4	8	3.4	176	2 OBR5B5_MOUSE	087505 mus musculu
5	8	3.4	204	2 O5NL46_ZYMO	05NL46 zymomonas m
6	8	3.4	232	2 O6W014_MAYDE	06W014 mayetiola d
7	8	3.4	232	2 O6W015_MAYDE	06W015 mayetiola d
8	8	3.4	234	2 O6W016_MAYDE	06W016 mayetiola d
9	8	3.0	51	2 O5BXY8_SCHJA	05BXY8 schistosoma
10	8	3.0	62	2 O5P2H2_AZOSE	05P2H2 azoarcus sp
11	8	3.0	68	1 RL29_ARCFU	028361 archaeeoglob
12	8	3.0	75	2 O9TIV0_TRIVU	09TIV0 trichosporus
13	8	3.0	75	2 O88460_MOUSE	088460 mus musculu
14	8	3.0	84	2 O5BHP9_MACMU	05BHP9 macaca mula
15	8	3.0	85	1 EGRF_MACMU	055245 macaca mula
16	8	3.0	88	2 O8AUI4_BACTN	08AUI4 bacteroides
17	8	3.0	88	2 O8IUI2_PLAF7	08IUI2 plasmodium
18	8	3.0	90	2 O69V62_ORYSA	069V62 oryza sativ
19	8	3.0	92	1 PETP_XANOR	059Y22 xanthomonas
20	8	3.0	93	2 O69W78_ORYSA	069W78 oryza sativ
21	8	3.0	96	2 O9LUI5_ORYSA	09LUI5 oryza sativ
22	8	3.0	99	2 O4Q4G7_LEIMA	04Q4G7 leishmania
23	8	3.0	99	2 O7VUI9_BORPE	07VUI9 bordetella
24	8	3.0	105	1 NIFW_ANASP	044149 anabaena sp
25	8	3.0	114	2 O5Q2X0_IDILO	05Q2X0 idiomarina
26	8	3.0	115	2 O5JDA2_PYRO	05JDA2 pyrococcus
27	8	3.0	117	2 O5JVO2_HUMAN	05JVO2 homo sapien
28	8	3.0	120	2 O9ZB4_STRCO	09ZB4 streptomyce
29	8	3.0	121	2 O8GSH5_ORYSA	08GSH5 oryza sativ
30	8	3.0	125	2 O7PLP6_DROME	07PLP6 drosophila
31	8	3.0	128	2 O6BXP3_DEBHA	06bxp3 debaromyce

105	6	2.6	58	2	Q64HJ5_MERVL	Q64HJ5_meleagrid h	178	6	2.6	88	2	Q7M1S4_CHLVU	Q7M1S4_chlorella v
106	2.6	61	2	Q6K8S7_ORYSA	Q6K8S7_oryza sativ	179	6	2.6	88	2	Q4RC42_TETNG	Q4RC42_tetradon n	
107	2.6	61	2	Q65583_9ALPH	Q65583_bovine hecp	180	6	2.6	89	2	Q657A8_ORYSA	Q657A8_oryza sativ	
108	2.6	61	2	Q4SX62_TETNG	Q4SX62_tetradon n	181	6	2.6	89	2	Q58PV5_BRWMA	Q58PV5_erwinia amy	
109	2.6	62	2	Q96FS0_HUMAN	Q96FS0_homo sapien	182	6	2.6	89	2	Q9Z4S3_SALTY	Q9Z4S3_salmonella	
110	2.6	62	2	Q4XD34_PLACH	Q4XD34_plasmodium	183	6	2.6	89	2	Q6NH88_CORDI	Q6NH88_corynebace	
111	2.6	63	2	Q8EN91_OCRBH	Q8EN91_oceanobacil	184	6	2.6	89	2	Q98HY8_RHILLO	Q98HY8_rhizobium l	
112	2.6	66	2	Q6AV31_ORYSA	Q6AV31_oryza sativ	185	6	2.6	89	2	Q7DJY7_9Z2ZZ	Q7DJY7_plasmod col	
113	2.6	66	2	Q8BV72_HUMAN	Q8BV72_homo sapien	186	6	2.6	89	2	Q11332_MCVI	Q11332_molnucum c	
114	2.6	67	2	Q9X3M1_PSEPU	Q9X3M1_pseudomonas	187	6	2.6	90	2	Q5OJJO_SALTY	Q5OJJO_salmonella	
115	2.6	68	2	Q5XNQ4_MANES	Q5XNQ4_manihot esp	188	6	2.6	90	2	Q9ZGS5_ECO57	Q9ZGS5_escherichia	
116	2.6	68	2	Q75HL5_ORYSA	Q75HL5_oryza sativ	189	6	2.6	90	2	Q8VAS5_MSV	Q8VAS5_white spot	
117	2.6	69	2	Q5ZSR0_ORYSA	Q5ZSR0_oryza sativ	190	6	2.6	91	2	TM10_DESHA	TM10_debaryomyce	
118	2.6	69	2	Q64913_LYCES	Q64913_lycopersico	191	6	2.6	91	2	Q96U75_NEUCR	Q96U75_neurospora	
119	2.6	69	2	Q83HD7_TROM8	Q83HD7_tropheryma	192	6	2.6	92	2	Q9HP62_HALSA	Q9HP62_halobacteri	
120	2.6	70	2	Q5JCTU6_ORYSA	Q5JCTU6_oryza sativ	193	6	2.6	92	2	Q56ZY0_ARATH	Q56ZY0_arabidopsis	
121	2.6	70	2	Q9RPS5_SALTY	Q9RPS5_salmonella	194	6	2.6	92	2	Q9KX34_PSEAB	Q9KX34_pseudomonas	
122	2.6	71	2	Q93M44_BORPE	Q93M44_bordetella	195	6	2.6	93	1	YGJ3_ERWCH	YGJ3_erwinia chr	
123	2.6	71	2	Q61J86_DROME	Q61J86_drosophila	196	6	2.6	93	2	Q64BZ1_9ARCH	Q64BZ1_uncultured	
124	2.6	72	2	Q7U685_SYMPX	Q7U685_synchococc	197	6	2.6	93	2	Q64DI6_9ARCH	Q64DI6_uncultured	
125	2.6	72	2	Q4V2C5_BURMA	Q4V2C5_burkholderi	198	6	2.6	93	2	Q69TI9_ORYSA	Q69TI9_oryza sativ	
126	2.6	72	2	Q7TDM6_SVIRU	Q7TDM6_haiovirus h	199	6	2.6	93	2	Q84DW8_TROMH	Q84DW8_tropheryma	
127	2.6	72	2	Q8V6U1_SVIRU	Q8V6U1_haiovirus h	200	6	2.6	94	1	VIXS_BRAPS	VIXS_bacteriophba	
128	2.6	73	2	Q8TVJ9_ANGGA	Q8TVJ9_anopheles g								
129	2.6	73	2	Q9KBP1_BACHD	Q9KBP1_bacillus ha								
130	2.6	73	2	Q9RCA0_BACHD	Q9RCA0_bacillus ha								
131	2.6	74	2	Q949H1_HORVU	Q949H1_hordeum vnl								
132	2.6	75	2	Q8RZS5_ORYSA	Q8RZS5_oryza sativ								
133	2.6	75	2	Q90160_NPYBM	Q90160_bombyx mori								
134	2.6	76	2	Q4RGD0_TETNG	Q4RGD0_tetradon n								
135	2.6	76	2	Q96MD3_9HYPO	Q96MD3_akantthomyce								
136	2.6	77	2	Q96MF8_9HYPO	Q96MF8_polyccephalo								
137	2.6	77	2	Q9NRK3_HUMAN	Q9NRK3_homo sapien								
138	2.6	77	2	Q6L0U6_XENLA	Q6L0U6_xenopus lae								
139	2.6	78	2	Q94Q10_SOLTU	Q94Q10_solanum tub								
140	2.6	78	2	Q4ZV49_PSESY	Q4ZV49_pseudomonas								
141	2.6	78	2	Q83EUT_COXBU	Q83EUT_coxiella bu								
142	2.6	78	2	Q83EUT_COXBU	Q83EUT_coxiella bu								
143	2.6	80	1	CX7A1_MOUSE	P56392_mus musculu								
144	2.6	80	2	Q8J2W6_PYPAB	Q8J2W6_pyrococcus								
145	2.6	80	2	Q4LSC7_9BORR	Q4LSC7_burkholderi								
146	2.6	80	2	Q8VH90_MASHI	Q8VH90_maetomyx hi								
147	2.6	80	2	Q8VH91_HYLA1	Q8VH91_hyalomyscus								
148	2.6	80	2	Q8VH92_MUSMI	Q8VH92_mus minutol								
149	2.6	80	2	Q8VH94_MUSPA	Q8VH94_mus pahari								
150	2.6	80	2	Q8VH95_MUSCO	Q8VH95_mus cookii								
151	2.6	80	2	Q8VH96_MUSCR	Q8VH96_mus caroli								
152	2.6	80	2	Q8VH97_MUSCE	Q8VH97_mus cervico								
153	2.6	80	2	Q8VH98_MUSCP	Q8VH98_mus capetus								
154	2.6	80	2	Q8VH99_MUSSI	Q8VH99_mus spicile								
155	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
156	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
157	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
158	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
159	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
160	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
161	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
162	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
163	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
164	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
165	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
166	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
167	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
168	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
169	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
170	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
171	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
172	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
173	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
174	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
175	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
176	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								
177	2.6	80	2	Q8VH99_MUSMA	Q8VH99_mus macedon								

```

CC Event=Alternative splicing; Named Isoforms=2;
CC Comment=The 2 isoforms differ functionally in their response to
CC phorbol ester: isoform JM-A is processed but not isoform JM-B.
CC So, they respectively represent cleavable and noncleavable forms
CC of the receptor. Both isoforms are expressed in cerebellum,
CC cerebral cortex, spinal cord, medulla oblongata and eye, but the
CC kidney expresses solely isoform JM-A and the heart solely
CC isoform JM-B;
CC Name=JM-A;
CC IsoId=Q61527-1; Sequence=Displayed;
CC Name=JM-B;
CC IsoId=Q61527-2; Sequence=VSP_002896;
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; I47241; AAA3534.1; -; mRNA.
CC DR Ensembl; ENSMUSG0000062209; Mus musculus.
CC MGI; MGI:104771; ErbB4.
CC DR GO; GO:0045165; P:cell fate commitment; IDA.
CC DR GO; GO:0007507; P:heart development; IMP.
CC DR GO; GO:0007399; P:neurogenesis; IMP.
CC DR InterPro; IPR000719; Prot kinase.
CC DR InterPro; IPR008266; Tyr kinase AS.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
CC DR PROSITE; PS00011; PROTEIN_KINASE_DOM; PARTIAL.
CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; PARTIAL.
CC DR Alternative splicing; ATP-binding; Kinase; Multigene family;
CC Nucleotide-binding; Phosphorylation; Receptor; Transferase;
CC KM Transmembrane; Tyrosine-protein kinase.
CC FT VARSPUBLIC 3 25 NQPTSHDCIYPTWGHSTLPQHA -> IGSISIDCIGLTD
CC (in isoform JM-B).
CC /FTid=VSP_002896.
CC FT NON CONS 27 28
CC FT NON TER 1 1
CC FT NON TER 95 95
CC SO SEQUENCE 95 AA; 10524 MW; BA3D0E99591744D8 CRC64;

Query Match 3.4%; Score 8; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AERYLVPO 53
DB 28 AERYLVPO 35

RESULT 2
082F38_STRAW PRELIMINARY; PRT; 145 AA.
ID 082F38_STRAW PRELIMINARY; PRT; 145 AA.
AC 082F38;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative RNA polymerase BCF-subfamily sigma factor.
GN Name=61938; OrderedLocustNames=SAV4425;
OS Streptomyces avermilti118.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=33903;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1073/pnas.211433198;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;

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RT *Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermilti118.";
RT Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NOCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT *Genome sequence of an industrial microorganism Streptomyces
RT avermilti118: deducing the ability of producing secondary
RT metabolites.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RL EMBL; BA000030; BAC72137.1; -; Genomic DNA.
DR HSSP; P34086; 10R7.
DR GO; GO:0016987; P:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007630; Sigma70_r4.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04545; Sigma70_r4; 1.
KM Complete proteome; DNA-binding; Transcription;
KM Transcription regulation.
SO SEQUENCE 145 AA; 15792 MW; 81AF896072574B55 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 PQPPSPRE 180
DB 3 PQPPSPRE 10

RESULT 3
06SA27_RHOSH PRELIMINARY; PRT; 160 AA.
ID 06SA27_RHOSH PRELIMINARY; PRT; 160 AA.
AC 06SA27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE R-Rest endonuclease.
GN Name=R-Rest;
OS Rhodospirillum rubrum (Rhodospirillum rubrum sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxId=1063;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RA Luoma K.D., Wilson G.G.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY461516; AAS19437.1; -; Genomic DNA.
DR GO; GO:0004519; P:endonuclease activity; IEA.
KM Endonuclease.
SO SEQUENCE 160 AA; 18649 MW; 665D7BAEBB10CFC CRC64;

Query Match 3.4%; Score 8; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAPSEGAG 108
DB 52 LAPSEGAG 59

RESULT 4
08R5B5_MOUSE PRELIMINARY; PRT; 176 AA.
ID 08R5B5_MOUSE PRELIMINARY; PRT; 176 AA.
AC 08R5B5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tor2a protein (Fragment).
GN Name=tor2a;
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gutaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalius D.E.,
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strubeberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023085; AAH23085.1; -; mRNA.
DR MGI; MGI:133596; Tor2a.
DR GO; GO:0005615; Cytoplasmic space; TMS.
DR InterPro; IPR010448; Torsin.
DR Pfam; PF06309; Torsin; 1.
DR NON TER
SQ SEQUENCE 176 AA; 19940 MW; 404F703101F4B64 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LGLEPSEE 94
DB 134 LGLEPSEE 141

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RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-Y., Um H.-W., Lee H.-J., Oh S.-D., Kim J.Y.,
RA Kang H.L., Lee S.-Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
DR EMBL; AB008692; AA950564.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 204 AA; 22120 MW; 58766D500A2D3C1A CRC64;

Query Match 3.4%; Score 8; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 PARRPAGA 191
DB 46 PARRPAGA 53

RESULT 6
O6M014 MAYDE PRELIMINARY; PRT; 232 AA.
ID O6M014 MAYDE PRELIMINARY;
AC O6M014;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Salivary secreted protein.
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Sciarioidea;
OC Cecidomyiidae; Mayetiola.
CX NCBI_TaxID=39758;
RN
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14871619; DOI=10.1016/j.jmb.2003.10.008;
RA Liu X., Fellera J.P., Wilde G.E., Stuart J.J., Chen M.S.;
RT "Characterization of two genes expressed in the salivary glands of the
RT Hessian fly, Mayetiola destructor (Say).";
RL Insect Biochem. Mol. Biol. 34:229-237(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chen M.-S., Fellera J.P.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY318788; AAC88248.1; -; mRNA.
SQ SEQUENCE 232 AA; 25436 MW; 1A732E80010DAC7 CRC64;

Query Match 3.4%; Score 8; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRSG 81
DB 104 RSSSTRSG 111

RESULT 7
O6M015 MAYDE PRELIMINARY; PRT; 232 AA.
ID O6M015 MAYDE PRELIMINARY;
AC O6M015;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Salivary secreted protein.
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Sciarioidea;
OC Cecidomyiidae; Mayetiola.
CX NCBI_TaxID=39758;
RN
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14871619; DOI=10.1016/j.jmb.2003.10.008;
RA Liu X., Fellera J.P., Wilde G.E., Stuart J.J., Chen M.S.;
RT "Characterization of two genes expressed in the salivary glands of the
RT Hessian fly, Mayetiola destructor (Say).";
RL Insect Biochem. Mol. Biol. 34:229-237(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Liu X., Fellera J.P.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY318788; AAC88248.1; -; mRNA.
SQ SEQUENCE 232 AA; 25436 MW; 1A732E80010DAC7 CRC64;

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RT Hessian fly, Mayetiola destructor (Say)."  
 RL Insect Biochem. Mol. Biol. 34:229-237(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chen M.-S., Fellers J.P.,  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY318787; AAC08247.1; -; mRNA.  
 SO SEQUENCE 232 AA; 25419 MW; 4F2FC5386601056A CRC64;

Query Match 3.4%; Score 8; DB 2; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRSG 81  
 DB 104 RSSSTRSG 111

## RESULT 8

06W016\_MAYDE PRELIMINARY; PRT; 234 AA.  
 AC 06W016;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Salivary secreted protein.  
 OS Mayetiola destructor (Hessian fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;  
 OC Cecidomyiidae; Mayetiola.  
 OX NCBI\_TaxId=39758;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Published=14871619; DOI=10.1016/j.jmb.2003.10.008;  
 RX Liu X., Fellers J.P., Wilde G.E., Stuart J.J., Chen M.S.,  
 RT "Characterization of two genes expressed in the salivary glands of the  
 Hessian fly, Mayetiola destructor (Say)."  
 RL Insect Biochem. Mol. Biol. 34:229-237(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chen M.-S., Fellers J.P.,  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY318786; AAC08246.1; -; Genomic DNA.  
 SO SEQUENCE 234 AA; 25664 MW; 9764921336ED7D6C CRC64;

Query Match 3.4%; Score 8; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRSG 81  
 DB 104 RSSSTRSG 111

## RESULT 9

05BX18\_SCHJA PRELIMINARY; PRT; 51 AA.  
 AC 05BX18;  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Hypoetical protein.  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxId=6182;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Han Z.,  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY81848; AAX2737.1; -; mRNA.  
 KW Hypoetical protein.  
 SO SEQUENCE 51 AA; 5540 MW; 1E27BAB016CB973B CRC64;

Query Match 3.0%; Score 7; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 PASPLDS 28  
 DB 5 PASPLDS 11

## RESULT 10

05P2H2\_AZOSE PRELIMINARY; PRT; 62 AA.  
 AC 05P2H2;  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Hypoetical protein.  
 GN OrderedLocustNames=AZOSEA23670; ORFNames=eba4183;  
 OS Azoarcus sp. (strain BbN1).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;  
 OC Rhodocyclaceae; Azoarcus.  
 OX NCBI\_TaxId=76114;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=BbN1;  
 RC PubMed=15551059; DOI=10.1007/s00203-004-0742-9;  
 RA Rabus R., Kube M., Heider J., Beck A., Heilmann K., Widdel P.,  
 RT Reinhardt R.,  
 RL "The genome sequence of an anaerobic aromatic-degrading denitrifying  
 bacterium, strain BbN1."  
 RT Arch. Microbiol. 183:27-36(2005).  
 DR EMBL; CR55306; CA108492.1; -; Genomic DNA.  
 KW Complete proteome; Hypoetical protein.  
 SO SEQUENCE 62 AA; 7272 MW; 194B330CA5F5B1A CRC64;

Query Match 3.0%; Score 7; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RSSSTRS 80  
 DB 17 RSSSTRS 23

## RESULT 11

RL29\_ARCFU STANDARD; PRT; 68 AA.  
 AC 028361;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE 50S ribosomal protein L29P.  
 GN Name=rpL29P; OrderedLocustNames=A1918;  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 OX NCBI\_TaxId=2234;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RC MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;  
 RX Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwin M.L., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kiehlavase A.R., Graham D.E., Kyriades N.C., Gill S.R.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., White O., Nelson K.E.,  
 RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,  
 RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodok A.,  
 RA Zhou L., Overbeek R., Gocayne J.D., Spriggs T., Artiach P., Kaine B.P.,  
 RA Uitterback T.R., Cotton M.D., Spillings T., Artiach P., Fujii C.,  
 RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,  
 RA Garland S.A., Mason T.M., Olsen G.V., Fraser C.M., Smith H.O.,  
 RA Woese C.R., Venter J.C.;

"The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon *Archaeoglobus fulgidus*.";  
 RL Nature 390:364-370(1997).  
 CC -1- SIMILARITY: Belongs to the ribosomal protein L29P family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC -----  
 CC EMBL; AE000971; AAB8356.1; -; Genomic\_DNA.  
 DR PIR; E69489; E69489.  
 DR TIGR; AF1918; -.  
 DR HAMAP; MF\_00374; -; 1.  
 DR InterPro; IPR001854; Ribosomal\_L29.  
 DR Pfam; PF00831; Ribosomal\_L29; 1.  
 DR TIGRFAMs; TIGR00012; L29; 1.  
 DR PROSITE; PS00579; RIBOSOMAL\_L29; 1.  
 KW Complete proteome; Ribonucleoprotein; Ribosomal protein.  
 SQ SEQUENCE 68 AA; 8010 MW; BF962BB601FF3A9 CRC64;  
 QY Query Match 3.0%; Score 7; DB 1; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 214 GGAVERN 220  
 38 GGAVERN 44  
 QY 214 GGAVERN 220  
 38 GGAVERN 44  
 RESULT 12  
 Q9TVV0 TRIVU PRELIMINARY; PRT; 75 AA.  
 ID Q9TVV0;  
 AC 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Type II gonadotrophin releasing hormone.  
 OS *Trichosurus vulpecula* (Brush-tailed possum).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.  
 NCBI\_TaxID=9337;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lawrence S.B., McNally K.P., Fidler A.E.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF193516; AAF07190.1; -; mRNA.  
 DR GO; GO:0005576; Extracellular region; IEA.  
 DR GO; GO:0005179; P.hormone activity; IEA.  
 DR GO; GO:0007275; P.development; IEA.  
 DR InterPro; IPR002012; GnRH.  
 DR Pfam; PF00446; GnRH; 1.  
 DR PROSITE; PS00473; GnRH; 1.  
 KW Hormone.  
 SQ SEQUENCE 75 AA; 8381 MW; 1C0E324492CA4283 CRC64;  
 QY Query Match 3.0%; Score 7; DB 2; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 88 GLEPSRE 94  
 42 GLEPSRE 48  
 QY 88 GLEPSRE 94  
 42 GLEPSRE 48  
 RESULT 13  
 O88460 MOUSE PRELIMINARY; PRT; 75 AA.  
 ID O88460;  
 AC 088460;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE EGF-like growth factor receptor ErbB4 intracellular domain  
 DE (Fragment).  
 GN Name=ErbB4;  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CD-1; TISSUE=Uterus;  
 RA Lim H., Das S.K., Dey S.K.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF059177; AAC28334.1; -; mRNA.  
 DR MGI; MGI:104771; ErbB4.  
 DR GO; GO:0045165; P:cell fate commitment; IDA.  
 DR GO; GO:0007507; P:heart development; IMP.  
 DR GO; GO:0007399; P:neurogenesis; IMP.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 75 75  
 SQ SEQUENCE 75 AA; 8371 MW; 718C044B67673A70 CRC64;  
 QY Query Match 3.0%; Score 7; DB 2; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 47 BEYLVPQ 53  
 2 BEYLVPQ 8  
 QY 47 BEYLVPQ 53  
 2 BEYLVPQ 8  
 RESULT 14  
 Q58HF9 MACMU PRELIMINARY; PRT; 84 AA.  
 ID Q58HF9;  
 AC 058HF9;  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Cut-like 1 (Fragment).  
 OS *Macca mulatta* (rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; OC Cercopithecidae; Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Roth C.L., Mastroianni C.A., Cabrera R., Mungenast A., Heger S., Jung H., Dubay C., Ojeda S.R.;  
 RL "Gene Expression Profiling of the Nonhuman Primate Hypothalamus at the Time of Female Puberty Reveals Activation of Tumor Suppressor."  
 RT Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY950560; AAX44002.1; -; mRNA.  
 FT NON\_TER 1 1  
 FT NON\_TER 84 84  
 SQ SEQUENCE 84 AA; 9190 MW; 57C48F764827B20 CRC64;  
 QY Query Match 3.0%; Score 7; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 102 APSEGAG 108  
 38 APSEGAG 44  
 QY 102 APSEGAG 108  
 38 APSEGAG 44  
 RESULT 15  
 EGFR MACMU STANDARD; PRT; 85 AA.  
 ID EGFR MACMU  
 AC P55245;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Epidermal growth factor receptor (EC 2.7.1.112) (Fragment).  
 GN Name=EGFR;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=95124501; PubMed=7545971;  
 RA Ma Y.J., Costa M.E., Ojeda S.R.;  
 RT "Developmental expression of the genes encoding transforming growth factor alpha and its receptor in the hypothalamus of female rhesus macaques";  
 RL Neuroendocrinology 60:346-359(1994).  
 CC -1 FUNCTION: The EGF receptor mediates the biological signal of EGF, and also of TGF-alpha, amphiregulin, heparin-binding EGF, Gp30 and vaccinia virus growth factor.  
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.  
 CC -1 SUBUNIT: Binds RIBK1. Part of a complex with ERBB2 and either PIK3C2A or PIK3C2B. The autophosphorylated form interacts with PIK3C2B, maybe indirectly (By similarity).  
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1 TISSUE SPECIFICITY: Hypothalamus.  
 CC -1 DEVELOPMENTAL STAGE: Levels in the medial basal hypothalamus and preoptic area are elevated during neonatal life (1 week-6 months), decrease during juvenile development (8-18 months) and markedly increase during the expected time of puberty (30-36 months).  
 CC -1 MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA synthesis, and cell proliferation.  
 CC -1 SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor subfamily.  
 CC -----  
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 CC -----  
 CC EMBL: S75916; AAB33095.1; -; mRNA.  
 CC F1R: I78540; I78540.  
 CC HSP: Q9H2C9; I14.  
 CC SWR: P55245; 1-85.  
 CC InterPro: IPR000719; Prot\_kinase.  
 CC InterPro: IPR001245; Tyr\_kinase.  
 CC InterPro: IPR008266; Tyr\_kinase\_AS.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC ProDom: PD000001; Prot\_kinase; 1.  
 CC PROSITE: PS00107; PROTEIN KINASE ATP; PARTIAL.  
 CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 CC PROSITE: PS00109; PROTEIN KINASE TYR; PARTIAL.  
 CC ATP-binding; Kinase; Nucleotide-Binding; Receptor; Transferase;  
 KW Tyrosine-protein kinase.  
 FT DOMAIN 1 77 Protein kinase.  
 FT NON\_TER 1 1  
 FT TER 85 85  
 FT SEQUENCE 85 AA; 9866 MW; D812DF47C23B3C18 CRC64;  
 SQ  
 Query Match 3.0%; Score 7; DB 1; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 MARDPR 11  
 DB 79 MARDPR 85

RESULT 16  
 Q8A014\_BACTN

ID Q8A014\_BACTN PRELIMINARY; PRT; 85 AA.  
 AC Q8A014;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=BT4037;  
 OS Bacteroides thetaiotaomicron.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 NCBI\_TaxID=818;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=VPI-5482 / ATCC 29148;  
 RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;  
 RA Xu J., Bjurell M.K., Hamrod J., Deng S., Carmichael L.K.,  
 RA Chiang H.C., Hooper L.V., Gordon J.I.;  
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";  
 RL Science 299:2074-2076(2003).  
 DR EMBL: AS016943; AA079142.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 85 AA; 9534 MW; 3A8BA1F1084BCA03 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 ASPLDST 29  
 DB 56 ASPLDST 62

RESULT 18

QY 121 AKGIQSL 127  
 DB 73 AKGIQSL 79  
 Query Match 3.0%; Score 7; DB 2; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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069V62. ORYSA
ID 069V62. ORYSA PRELIMINARY; PRT; 90 AA.
AC 069V62. 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0556B08.12.
GN Name=P0556B08.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0556B08."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004279; BADJ5616.1; -; Genomic_DNA.
DR Gramene; O69V62; -;
KM Hypothetical protein.
SQ SEQUENCE 90 AA; 10041 MW; 2EAB58B4FC60FB5 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 PRSPLAP 103
Db 54 PRSPLAP 60

RESULT 19
FETP_XANOR STANDARD; PRT; 92 AA.
ID 05GY22;
AC 05GY22;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=XO03145;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673718; DOI=10.1093/nar/gki1206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
the bacterial blight pathogen of rice."
RL Nucleic Acids Res 33:577-586(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; AE013598; AAW76399.1; ALT_INT; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.

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DR ProDom; PD029191; DUF495; 1.
KM Complete Proteome; Iron.
SQ SEQUENCE 92 AA; 10661 MW; 5793BA0309452383 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 DGYVAPL 157
Db 83 DGYVAPL 89

RESULT 20
069WY8. ORYSA
ID 069WY8. ORYSA PRELIMINARY; PRT; 93 AA.
AC 069WY8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein P0417G12.5 (Hypothetical protein
P0429G06.22)
GN Name=P0417G12.5; Synonyms=P0429G06.22;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0429G06."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0429G06."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003711; BADJ5549.1; -; Genomic_DNA.
DR EMBL; AP003626; BADJ5517.1; -; Genomic_DNA.
DR Gramene; O69WY8; -;
KM Hypothetical protein.
SQ SEQUENCE 93 AA; 8342 MW; CD146848A7B6E831 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 PAPGAGG 67
Db 44 PAPGAGG 50

RESULT 21
09LJ15. ORYSA
ID 09LJ15. ORYSA PRELIMINARY; PRT; 96 AA.
AC 09LJ15;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein P0667A10.13.
GN Name=P0667A10.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,

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RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
RA Htjshita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
RA Katsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Nakai Y.,  
RA Nagasaki H., Nakashima M., Nakama Y., Nakemichi Y., Nakamura M.,  
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Teresawa K., Tsuji K.,  
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinaka R., Yukawa K.,  
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.T., Eun M.Y.,  
RA Yano M., Jiang J., Gotohori T.;  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
DR EMBL: AB001073; BAA89575.1; -; Genomic\_DNA.  
DR Gramene; O9LJ15; -;  
KW Hypochemical protein.  
SQ SEQUENCE 96 AA; 9606 MW; 2AC6441717D52FP CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 77 STRSGG 83  
DB 59 STRSGG 65  
RESULT 22  
O404G7 LEIMA PRELIMINARY; PRT; 99 AA.  
AC O404G7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE Hypochemical protein.  
GN ORFNames=lmjF33\_0420;  
OS Leishmania major.  
OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RX (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Frledlin;  
RA Beacock C.S., Murphy L., Ivens A.C., Bertman M., Blackwell J.,  
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,  
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrett B.G.;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
RM EMBL: CT005270; CAJ05987.1; -; Genomic\_DNA.  
KW Hypochemical protein.  
SQ SEQUENCE 99 AA; 10713 MW; 82P2A39B24975BB4 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 225 POGGAAP 231  
DB 87 POGGAAP 93  
RESULT 23  
O7VU19 BORPE PRELIMINARY; PRT; 99 AA.  
AC O7VU19;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative exported protein.  
GN OrderedLocustNames=BP3099;  
OS Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
OX NCBI\_TaxID=520;

RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;  
RC MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
RX Parkhill J., Sebatina M.T., Preston A., Murphy L.D., Thomson N.R.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,  
RA Leather S., Mole S., Noberezak H., O'Neill S., Ormond D., Price C.,  
RA Rabbintowitach B., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrett B.G., Maekell D.J.;  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica.";  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL: BX64020; CAB43367.1; -; Genomic\_DNA.  
DR Complete proteome.  
SQ SEQUENCE 99 AA; 9995 MW; 7F3C417E0B36BA25 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 184 PAARPAG 190  
DB 64 PAARPAG 70  
RESULT 24  
N1FW ANASP STANDARD; PRT; 105 AA.  
AC O441I9;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Nitrogenase stabilizing/protective protein n1fw.  
GN Name=n1fw; OrderedLocustNames=a111433;  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RX (1)  
RP NUCLEOTIDE SEQUENCE.  
RC Bulkema W.J., Scarpino L.A., Haselkorn R.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Tabata S.,  
RA Yasuda M., Sugimoto M., Takazawa M., Yamada M.,  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
RT cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
CC -1- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative  
CC damage (By similarity).  
CC -1- SUBUNIT: Homotrimer; associates with n1fd (By similarity).  
CC -1- SIMILARITY: Belongs to the n1fw family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL: U47055; AA87952.1; -; Genomic\_DNA.  
CC EMBL: BA000019; BAB73390.1; -; Genomic\_DNA.  
CC PIR: AF1985; AF1985.  
CC HAMAP: MF\_00529; -; 1.  
CC InterPro: IPR004893; N1fw.

DR Pfam; PF03206; M1FW; 1.  
KM Complete proteome; Nitrogen fixation.  
SQ SEQUENCE 105 AA; 12262 MW; 498DF9B8ADB9B95F CRC64;  
Query Match 3.0%; Score 7; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 43 LYDAEY 49  
DB 11 LYDAEY 17  
RESULT 25  
OSQZX0 IDILO PRELIMINARY; PRT; 114 AA.  
ID OSQZX0;  
AC 01-FEB-2005 (TREMBLrel. 29, Created)  
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)  
DE 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
DE Transposase Tra5 related protein.  
DE Name=tra5\_2; OrderedlocusNames=IL0051;  
OS Idiomarina loihiensis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Idiomarinaceae; Idiomarina.  
OX NCBI\_TaxID=135577;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=L2-TR / DSM 15497 / ATCC BAA-735;  
RX PubMed=15596722; DOI=10.1073/pnas.0407638102;  
RA Hou S., Saw J.H., Lee K.S., Freitas T.A., Belisle C., Kawarabayashi Y.,  
RA Donachie S.P., Pltkin A., Galperin M.Y., Koonin E.V., Makarova K.S.,  
RA Omelchenko M.V., Sorokin A., Wolf Y.I., Li Q.X., Keum Y.S.,  
RA Campbell S., Denery J., Aizawa S.-I., Shibata S., Malhotra A.,  
RA Alam M.;  
RT "Genome sequence of the deep-sea gamma-proteobacterium Idiomarina  
RT loihiensis reveals amino acid fermentation as a source of carbon and  
RT energy.";  
RT Proc. Natl. Acad. Sci. U.S.A. 101:18036-18041 (2004).  
DR EMBL; AE017340; MAAV80895.1; -; Genomic\_DNA.  
KM Complete proteome.  
SQ SEQUENCE 114 AA; 12952 MW; 1C31899E1841D187 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 184 PAAPAG 190  
DB 83 PAAPAG 89  
RESULT 26  
OSJDA2 PYRKO PRELIMINARY; PRT; 115 AA.  
ID OSJDA2;  
AC 05JDA2;  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE SNOBNP component, Gar1 homolog.  
DE OrderedlocusNames=TK2286;  
GN Pyrococcus kodakarensis (Thermococcus kodakarensis).  
OS Pyrococcus kodakarensis; Thermococci; Thermococcales; Thermococcaceae;  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=69014;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=KOD1;  
RX PubMed=15710748; DOI=10.1101/gr.3003105;  
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;  
RT "Complete genome sequence of the hyperthermophilic archaeon  
RT Thermococcus kodakarensis KOD1 and comparison with Pyrococcus  
RT genomes.";

RL Genome Res. 15:352-363(2005).  
DR EMBL; AP006878; BAD86475.1; -; Genomic\_DNA.  
KM Complete proteome.  
SQ SEQUENCE 115 AA; 12737 MW; AA2ED15F21AC7D84 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 GVKDVF 211  
DB 39 GVKDVF 45  
RESULT 27  
OSJVO2 HUMAN PRELIMINARY; PRT; 117 AA.  
ID OSJVO2;  
AC OSJVO2;  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE OTTHUMP000000474 (Fragment).  
GN ORFNames=RP11-176F3.6-003;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tacey A.;  
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL139113; CA139660.1; -; Genomic\_DNA.  
FT NON TER  
SQ SEQUENCE 117 AA; 12034 MW; DA7B8F90E5ACFP08 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 173 POPSPR 179  
DB 93 POPSPR 99  
RESULT 28  
OSZBF4 STRCO PRELIMINARY; PRT; 120 AA.  
ID OSZBF4;  
AC OSZBF4;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE Putative regulatory protein.  
DE OrderedlocusNames=SC06459; ORFNames=SC9B5.26c;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
OC Streptomyces; Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kiese T., Larke L., Murphy L.D., Oliver K., O'Neil S.,  
RA Rabinovitch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";

RL Nature 417:141-147(2002).  
DR EMBL: AL939127; CAA22768.1; -; Genomic\_DNA.  
DR PIR: T35946; T35946.  
DR HSSP: P30340; ISMT.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO: GO:0006350; P:transcription; IEA.  
DR InterPro: IPR001845; HTH\_ArSR.  
DR InterPro: IPR011991; Wing\_hlx\_DNA\_bd.  
DR Pfam: PF01022; HTH\_5; 1.  
DR PRINTS: PRO0778; HTHARSR.  
DR SMART: SM00418; HTH\_ArSR.1.  
DR PROSITE: PSS0987; HTH\_ArSR\_2; 1.  
DR Cadmus: resistance; Complete proteome; DNA-binding; Transcription;  
KW transcription regulation.  
SQ SEQUENCE 120 AA; 12840 MW; C345598BB098D423 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 179 RESPLA 185  
|||  
46 RESPLA 52  
  
RESULT 29  
OEGSH5 ORYSA PRELIMINARY; PRT; 121 AA.  
ID OEGSH5 ORYSA PRELIMINARY;  
AC OEGSH5;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
DE Hypothetical protein P0418E08.129 (Hypothetical protein  
GN OJ1341 A08.107).  
DN Name:P0418E08.129; Synonyms:OJ1341 A08.107;  
OS Oryza sativa (Japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa japonica (CA3) genomic DNA, chromosome 7, BAC  
clone:OJ1341 A08.";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP004382; BAC16086.1; -; Genomic DNA.  
DR EMBL: AP003754; BAC30199.1; -; Genomic DNA.  
DR Gramene; OEGSH5; -;  
KW Hypothetical protein.  
SQ SEQUENCE 121 AA; 12512 MW; 1E104206D3A7FDB8 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 97 PRSPLA 103  
|||  
72 PRSPLA 78  
  
RESULT 30  
O7PLP6 DROME PRELIMINARY; PRT; 125 AA.  
ID O7PLP6 DROME PRELIMINARY;  
AC O7PLP6;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE CG40207-PA.3.  
GN ORFNames=CG40207;  
OS Drosophila melanogaster (Fruit fly).  
OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Eukaryota; Enderozoa; Ecdysozoa; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Friese E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacilic J.M., Park S., Pfeiffer B.D., Richardson S., Sodergren E.J.,  
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426071; PubMed=12537574;  
RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,  
RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,  
RA Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,  
RA Karpen G.H.;  
RT "Heterochromatic sequences in a Drosophila whole-genome shotgun  
assembly."  
RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Adams M.D., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G.,  
RA Li P.W., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D.,  
RA Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., An H.J., Baxendale J.,  
RA Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J.,  
RA Beasley E.M., Beeson K.Y., Bhandari D., Bolanos R.A., Busam D.A.,  
RA Center A., Chandra I., Dahlke C., Davenport L.B., Davies P.,  
RA Delcher A., Deng Z., Dew I., Dietz S.M., Dodson K.,  
RA Doup L.E., Dunn P., Evangelista C.C., Ferrieres S., Flanagan M.J.,  
RA Foster C., Gabrielian A.B., Gary N.S., Glasser K., Glodek A., Gong F.,  
RA Gu Z., Guan P., Halpern A.L., Harris M., Heiman T.J., Houck J.,  
RA Hoslin D., Howland T.J., Wei M.H., Ibegwan C., Jalali M., Kalish F.,  
RA Ke Z., Ketchum K.A., Kodira C.D., Kraft C., Kravitz S., Lai Z.,  
RA Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu J.R.,  
RA Maizels B., McIntosh T.C., McPherson D., Merkulov G., Miller J.R.,  
RA Milshina N.V., Mobarry C., Moy M., Murphy B., Nelson K.A.,  
RA Nuskearn D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reinert K.,  
RA Remington K., Scheeler F., Shue B.C., Siden-Kiamos I., Simpson M.,  
RA Skupski M.P., Smith T., Spier E., Strong R., Sun B., Tector C.,  
RA Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Williams S.M.,  
RA Woodage T., Wu D., Yao Q.A., Ye J., Zaveri J.S., Zhan M., Zhang G.,  
RA Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X.,  
RA Smith H.O., Myers E.W., Venter J.C.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Smith C.D., Acevedo D., Carlson J.W., Hoskins R.A., Kennedy C.,  
RA Mungall C.J., Yandell M.D., Celniker S.E., Karpen G.H.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB001002422; EAA46276.1; -; Genomic DNA.  
DR Ensembl: CG40207; Drosophila melanogaster.  
SQ SEQUENCE 125 AA; 13549 MW; A574074BB2A1B54 CRC64;  
  
Query Match 3.0%; Score 7; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 182 PLPAP 186  
|||  
29 PLPAP 35

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RESULT 31
O6BXP3 DEBHA PRELIMINARY; PRT; 128 AA.
ID O6BXP3 DEBHA PRELIMINARY; PRT; 128 AA.
AC O6BXP3 DEBHA PRELIMINARY; PRT; 128 AA.
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Debaryomyces hanseii chromosome B of strain CBS767 of Debaryomyces
DE hanseii.
GN Ordered locus names=DEBHA013649;
OS Debaryomyces hanseii (yeast) (Torulaepora hanseii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 7677;
RX PubMed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissarie A., Boyer J., Catolico L., Confanieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Leseur I., Ma L., Müller H.,
RA Nicoud J.-M., Nikolaki M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Sureau A.,
RA Szeuven D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudon B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RU Nature 430:35-44(2004).
DR EMBL; CR382134; CNG85011.1; -; Genomic_DNA.
DR InterPro; IPR005341; UPF0108.
DR Pfam; PF03656; Paml6; 1.
DR ProDom; PD311402; UPF0108; 1.
KM Complete proteome.
SQ SEQUENCE 128 AA; 13894 MW; D2844494C5E1BD35 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 TPOGGA 230
DB 35 TPOGGA 41

RESULT 32
O6D9H7 ERWCT PRELIMINARY; PRT; 131 AA.
ID O6D9H7 ERWCT PRELIMINARY; PRT; 131 AA.
AC O6D9H7 ERWCT PRELIMINARY; PRT; 131 AA.
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative membrane protein.
GN Ordered locus names=ECM0638;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holava M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Nordberg H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

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RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RU Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG73553.1; -; Genomic_DNA.
DR InterPro; IPR011309; UCP009726.
DR PIRSF; PIRSF009726; UCP009726; 1.
KM Complete proteome.
SQ SEQUENCE 131 AA; 14322 MW; 4A94397D34B150A7 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSLIED 38
DB 123 RSLIED 129

RESULT 33
O6YV89 9CAUD PRELIMINARY; PRT; 135 AA.
ID O6YV89 9CAUD PRELIMINARY; PRT; 135 AA.
AC O6YV89 9CAUD PRELIMINARY; PRT; 135 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Hypothetical VMB.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95336309; PubMed=7611876;
RA Anne J., Piten P., Van Mellaert L., Joris B., Odenakker G.,
RA Eysen H.;
RT "Analysis of the open reading frames of the main capsid proteins of
RT actinophage VMB.";
RU Arch. Virol. 140:1033-1047(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9908696; PubMed=9884227;
RA Van Mellaert L., Mel L., Lammerlyn E., Schacht S., Anne J.;
RT "Site-specific integration of bacteriophage VMB genome into
RT Streptomyces venezuelae and construction of a VMB-based integrative
RT vector.";
RU Microbiology 144:3351-3358(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91037942; PubMed=2230721;
RA Anne J., Van Mellaert L., Decock B., Van Damme J., Van Aerschoot A.,
RA Herdewijn P., Eysen H.;
RT "Further biological and molecular characterization of actinophage
RT VMB.";
RU J. Gen. Microbiol. 136:1365-1372(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15629775; DOI=10.1016/j.virol.2004.10.028;
RA Van Deesel W., Van Mellaert L., Lieegang H., Raach C.,
RA De Keersmaeker S., Geukens N., Lammerlyn E., Streit W., Anne J.;
RT "Complete genomic nucleotide sequence and analysis of the temperate
RT bacteriophage VMB.";
RU Virology 331:325-337(2005).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Van Deesel W., Van Mellaert L., Raach C., Lieegang H., Streit W.,
RA Anne J.;
RT "Nucleotide sequence analysis of Streptomyces venezuelae bacteriophage
RT VMB.";
RU (in) Unknown A. (eds.);
MICROBIAL IMMUNE EVASION STRATEGIES: MEETING OF THE BELGIAN SOCIETY
FOR MICROBIOLOGY, pp.30-30, Unknown Publisher (2003).
RN [6]

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RP NUCLEOTIDE SEQUENCE.  
 RA Anne J.F.C.;  
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.  
 RN (7)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Van Meillaert L.M.G.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN (8)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Van Dessel W., Van Meillaert L., Raasch C., Liesegang H., Streitt W.,  
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY320035; AAR29748.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14696 MW; 40B13987CA4DD477 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 PASPLDS 28  
 DB 60 PASPLDS 66

RESULT 34  
 Q7UR6\_RHOBA  
 ID Q7UR6\_RHOBA PRELIMINARY; PRT; 135 AA.

AC Q7UR6;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=RB3125;  
 OS Rhodospirillum rubrum.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 OC NCBI\_TaxID=117;  
 OK (1)  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=1;  
 RX MEDLINE=2735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardoc T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Heltmann K., Rabus R.,  
 RA Schiesner H., Mann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 RT strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
 DR EMBL; BX294138; CAD73011.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14862 MW; 83B9F9FCBA53DPF2 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RSGGCDL 85  
 DB 108 RSGGCDL 114

RESULT 35  
 Q75T02\_RABIT  
 ID Q75T02\_RABIT PRELIMINARY; PRT; 136 AA.

AC Q75T02;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Interleukin adhesion molecule-1 (Fragment).  
 GN Name=ICAM-1;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

OC Oryctolagus.  
 OK NCBI\_TaxID=9986;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Murata T.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB128157; BAD04920.1; -; mRNA.  
 FT NON TER 1 136 136  
 SQ SEQUENCE 136 AA; 14755 MW; 42EC3FPA18CB2B23 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SSSTRSG 81  
 DB 108 SSSTRSG 114

RESULT 36  
 O67TP2\_ORYSA  
 ID O67TP2\_ORYSA PRELIMINARY; PRT; 136 AA.

AC O67TP2;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Hypothetical protein B1342C04.50 (Hypothetical protein  
 DE B1045B05.3).  
 GN Name=B1342C04.50; Synonym=B1045B05.3;  
 OS Oryza sativa (Japanese cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Rharioideae; Oryzaceae; Oryza.  
 OK NCBI\_TaxID=39947;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Katayose Y.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC  
 RT clone:B1342C04.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Katayose Y.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC  
 RT clone:B1045B05.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP006057; BAD38479.1; -; Genomic DNA.  
 DR EMBL; AP005891; BAD38365.1; -; Genomic DNA.  
 DR Gramene; O67TP2;  
 KW Hypothetical protein.  
 SQ SEQUENCE 136 AA; 14817 MW; CF4D7ACADA37386 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 AARPAGA 191  
 DB 32 AARPAGA 38

RESULT 37  
 O699F3\_9HIV1  
 ID O699F3\_9HIV1 PRELIMINARY; PRT; 137 AA.

AC O699F3;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Gag protein (Fragment).  
 GN Name=gag;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=01CM2213;
RX PubMed=15577423;
RA Ndembi N., Takehisa J., Zekeng L., Kobayashi E., Nganop C.,
  Songok E.M., Kageyama S., Takemura T., Ido E., Hayami M., Kapteue L.,
  Ichimura H.;
RA "Genetic Diversity of HIV Type 1 in Rural Eastern Cameroon.";
RT J. Acquir. Immune Defic. Syndr. 37:1641-1650(2004).
RL EMBL; AY539583; AAT1000.1; -; Genomic_DNA.
DR SMR; O699F3; 3-81.
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR GO; GO:0046872; P:metal ion binding; IEA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR00721; Gag_p24.
DR InterPro; IPR01878; Znf_CCHC.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNRNGR.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
KM Core protein; Metal-binding; zinc; Zinc-finger.
PT NON_TER
PT 1 137 137
SQ SEQUENCE 137 AA; 15329 MW; 21BB33CEDC893BE CRC64;

Query Match 3.0%; Score 7; DB 2; Length 137;
Best Local Similarity 100.0%; Pred.No.2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AGATLIER 195
DB 69 AGATLIER 75

RESULT 38
Q97JX6_CLOAB PRELIMINARY; PRT; 138 AA.
ID Q97JX6;
AC 097JX6;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein CAC1147.
GN OrderedLocNames=CAC1147.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
  Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=2159325; PubMed=1466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Gibson J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
  Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille F.,
  Dally M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
  bacterium Clostridium acetobutylicum.";
RT J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007631; AAK79119.1; -; Genomic_DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 138 AA; 16453 MW; 99A7841D39ADE687 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred.No.2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LGIEPSE 93

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DB 37 LGIEPSE 43

RESULT 39
Q811Y7_PLAF7 PRELIMINARY; PRT; 140 AA.
ID Q811Y7;
AC Q811Y7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF11_0015;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Bertram M., Hyman R.W.,
  Carlton J.M., Patil A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
  Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
  Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
  Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
  Martin D.M.A., Fairlamb A.H., Fraunholz M.U., Roos D.S., Ralph S.A.,
  McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
  Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
  Fraser C.M., Barrett B.G.;
RA "Genome sequence of the human malaria parasite Plasmodium
  falciparum.";
RT Nature 419:498-511(2002).
RL EMBL; AE014836; AAN5612.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 140 AA; 16578 MW; 1B1CF83FDB15EAF6 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred.No.2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AKGLQSL 127
DB 125 AKGLQSL 131

RESULT 40
Q8XQW8_RALSO PRELIMINARY; PRT; 142 AA.
ID Q8XQW8_RALSO
AC Q8XQW8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE PROBABLE PROLINE RICH TRANSMEMBRANE PROTEIN.
GN OrderedLocNames=RS01194; ORFNames=RS01138;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
  Burkholderia; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangot S.,
  Arlat M., Billault A., Brottier P., Camus J.C., Cartolico L.,
  Chandler M., Choisne N., Claudel-Renard C., Cunac S., Demange N.,
  Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
  Sigler P., Trebault P., Whalen M., Wincker P., Levy M.,
  Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
RL EMBL; AL646083; CAD18345.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005590; DUF333.

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DR Pfam; PF03691; DUF333; 1.  
KW Complete proteome; Plasmid; Transmembrane.  
SQ SEQUENCE 142 AA; 14319 MW; 7A55E24890EDF441 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 142;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 77 STRSGGG 83  
DB 111 STRSGGG 117  
RESULT 41  
ID Q51IG9\_ENTH1 PRELIMINARY; PRT; 148 AA.  
AC Q51IG9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
OS Entamoeba histolytica HM-1:IMSS.  
GN ORFNames=102.f00008;  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxId=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS;  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Lofthus B., Anderson I., Davies R., Alemark U.C., Samuelson J.,  
RA Amedeo P., Roncaglia P., Bertman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipe M.,  
RA Hofer M., Bruchhaus I., Willhoet U., Bhattacharya A.,  
RA Chillingworth T., Churcher K., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
RA Quail M.A., Rabinowitch E., Norbertczak H., Price C., Wang Z.,  
RA Guillen N., Glickstein C., Stroup S.B., Bhattacharya S., Lohia A.,  
RA Foster P.G., Stiehlitz-Ponten T., Weber C., Singh U., Mukherjee C.,  
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
RA Fraser C.M., Hall N.;  
RL "The genome of the prokaryotic parasite Entamoeba histolytica.";  
RT Nature 433:865-868(2005).  
CC -1- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; AAFB01000364; EAL47492.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 148 AA; 17319 MW; 6D0803B90F057FDE CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 148;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 78 TRSGGGD 84  
DB 22 TRSGGGD 28  
RESULT 42  
ID Q5NUT6\_9ACTO PRELIMINARY; PRT; 155 AA.  
AC Q5NUT6;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein ORF155.  
GN Name=ORF155;  
OS Streptomyces albulus.  
OC Plasmid pNO33.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxId=68570;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=IFO 14147;  
RA Kawai T., Inoue S.;  
RT "Complete sequence of the plasmid pNO33 from Streptomyces albulus  
IFO14147.";  
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB058947; BAD80773.1; -; Genomic\_DNA.  
DR GO; GO:0003677; rDNA binding; IEA.  
DR GO; GO:0006355; P-regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001187; HTH\_3.  
DR Pfam; PF01381; HTH\_3; 2.  
DR SMART; SM00530; HTH\_XRB; 2.  
DR PROSITE; PSS0943; HTH\_CROCI; 2.  
KW Hypothetical protein; Plasmid.  
SQ SEQUENCE 155 AA; 16884 MW; 5687DEB1FE53DC2F CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 155;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 101 LAPSGGA 107  
DB 68 LAPSGGA 74  
RESULT 43  
ID Q5F4Y1\_NEIG1 PRELIMINARY; PRT; 161 AA.  
AC Q5F4Y1;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN OrderedAcusNames=NGO2162;  
OS Neisseria gonorrhoeae (Strain ATCC 700825 / FA 1090).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxId=242231;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RA Lewis L.A., Gillaespy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,  
RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,  
RA Song L., Lin S., Yuan X., Najaf F., Zhan F., Ren Q., Zhu H., Qi S.,  
RA Kenion S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;  
RT "The complete genome sequence of Neisseria gonorrhoeae.";  
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB004969; AAM90756.1; -; Genomic\_DNA.  
DR InterPro; IPR004027; SEC\_C\_motif.  
DR Pfam; PF02810; SEC\_C; 2.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 161 AA; 18035 MW; ACFB74F0A12B5877 CRC64;  
Query Match 3.0%; Score 7; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 141 DPTVPLP 147  
DB 129 DPTVPLP 135  
RESULT 44  
ID Q65WMO\_MANSW PRELIMINARY; PRT; 161 AA.  
AC Q65WMO;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
GN OrderedAcusNames=MS0033;  
OS Mannheimia succiniciproducens (Strain MBE155E).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Mannheimia.

OK NCBI\_TaxID=221988;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15378067; DOI=10.1038/nbt1010;  
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
 RA Kim C.H., Jeong H., Hur C.G., Kim J.U.,  
 RT "The genome sequence of the capnophilic rumen bacterium *Mannheimia*  
 RT *succiniciproducens*,"  
 RL Nat. Biotechnol. 22:1275-1281(2004).  
 DR EMBL, AB016827; AAU36640.1; -; Genomic\_DNA.  
 DR InterPro, IPR004027; SEC\_C\_motif.  
 DR Pfam, PF02810; SEC\_C\_2.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 161 AA; 18249 MW; B371B2C548B9DE91 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 141 DPTVPLP 147  
 DB 133 DPTVPLP 139  
 RESULT 45  
 OGH8T1 ORYSA PRELIMINARY; PRT; 164 AA.  
 ID OGH8T1 ORYSA PRELIMINARY;  
 AC OGH8T1  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DR Hypothetical protein OJ1523\_A02.9.  
 GN Name=OJ1523\_A02.9;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,  
 RA Overton I.L., Teltzin T., Kim M.W., Bera J.U., Jin S.S.,  
 RA Padrosh D.W., Tallon L.J., Koo H., Zilmann V., Hsiao J., Blunt S.,  
 RA Vanden S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,  
 RA Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,  
 RA White O., Salzberg S.L., Fraser C.M.,  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell R.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AC090874; AAN08215.1; -; Genomic\_DNA.  
 DR Gramene, OGH8T1;  
 DR GO, GO:0005489; F:electron transporter activity; IEA.  
 DR GO, GO:0006118; P:electron transport; IEA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 164 AA; 17643 MW; 0932D550E724E717 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 72 RHRSSST 78  
 DB 120 RHRSSST 126  
 RESULT 46  
 OS7P2 9TRYP  
 ID OS7P2 9TRYP PRELIMINARY; PRT; 165 AA.  
 AC OS7P2;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE Ecotin, putative.  
 GN ORFNames=TB927.5.1730;  
 OS Trypanosoma brucei.  
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5691;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GUrat10.1;  
 RA Ghedin E., Blandin G., Bartholomeu D., Caler B., Haas B., Hannick L.,  
 RA Shalom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,  
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,  
 RA Khialak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,  
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GUrat10.1;  
 RA El-Sayed N.M., Khialak H., Adams M.D.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GUrat10.1;  
 RA Haas B., Blandin G., El-Sayed N.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 KW EMBL, AC104617; AAX79124.1; -; Genomic\_DNA.  
 SQ SEQUENCE 165 AA; 19342 MW; EE06716BEE515476 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 175 PPSREG 181  
 DB 33 PPSREG 39  
 RESULT 47  
 O6NIG2 CORDI PRELIMINARY; PRT; 167 AA.  
 ID O6NIG2 CORDI PRELIMINARY;  
 AC O6NIG2  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DR Hypothetical protein.  
 GN OrderedLocusNames=DIP0813;  
 OS Corynebacterium diptheriae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=1717;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Biotype gravus / NCTC 13129;  
 RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;  
 RA Cerdano-Tarraga A.-M., Bistratou A., Dover L.G., Holden M.T.G.,  
 RA Pallen M.J., Bentley S.D., Beera G.S., Churcher C.M., James K.D.,  
 RA De Zuyra A., Chillingworth T., Cronin A., Dowd L., Fellwell T.,  
 RA Hamlin N., Holtroyd S., Jagels K., Moule S., Quail M.A.,  
 RA Rabinowitch E., Rutherford K.M., Thomson N.R., Unwin L.,  
 RA Whitehead S., Barrett B.G., Parkhill J.,  
 RT "The complete genome sequence and analysis of *Corynebacterium*  
 RT *diptheriae* NCTC13129,"  
 RL Nucleic Acids Res. 31:6516-6523(2003).  
 DR EMBL, BX248356; CAB49331.1; -; Genomic\_DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 167 AA; 18627 MW; 48F57F331105DCD0 CRC64;  
 Query Match 3.0%; Score 7; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 101 LAPSEGA 107

Db 53 LAPSEGA 59

## RESULT 48

ID Q6NMZ6\_BDEBA PRELIMINARY; PRT; 168 AA.

AC Q6NMZ6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Flagellar protein Flil.

GN Name=flil; OrderedLocustNames=Bdl076;

OS Bdellovibrio bacteriovorus.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;

OC Bdellovibrionaceae; Bdellovibrio.

NCBI\_TaxId=959;

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;

RX PubMed=14752164; DOI=10.1126/science.1093027;

RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,

RA Sockett R.E., Schuster S.C.;

RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a

RT genomic perspective.";

RL Science 303:689-692(2004).

DR EMBL; BX4248; CAE79003.1; -, Genomic DNA.

DR GO; GO:0009425; C:flagellar basal body (sensu Bacteria); IEA.

DR GO; GO:0006935; P:chemotaxis; IEA.

DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.

DR InterPro: IPR005503; F1L1.

DR Pfam: PF03748; F1L1; 1.

KM Complete proteome; Flagellum.

SQ SEQUENCE 168 AA; 18796 MW; 23842DC8E920E15 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 168;

Best Local Similarity 100.0%; Pred. No. 2, 9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 GVVKDVP 211

DB 155 GVVKDVP 161

## RESULT 49

ID Q5W9T4\_CHLRE PRELIMINARY; PRT; 175 AA.

AC Q5W9T4;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Lhc-like protein Lhl1.

GN Name=lhl1;

OS Chlamydomonas reinhardtii.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;

OC Chlamydomonadales; Chlamydomonadales; Chlamydomonas.

NCBI\_TaxId=3055;

RN NUCLEOTIDE SEQUENCE.

RP PubMed=15509845; DOI=10.1093/pcp/pch157;

RX Teramoto H., Itoh T., Ono T.;

RT "High-Intensity-Light-Dependent and Transient Expression of New Genes

RT Encoding Distant Relatives of Light-Harvesting Chlorophyll-a/b

RT Proteins in Chlamydomonas reinhardtii.";

RL Plant Cell Physiol. 45:1221-1232(2004).

DR EMBL; AB159046; BAB67134.1; -, mRNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0009765; P:photosynthesis light harvesting; IEA.

DR InterPro: IPR001344; Chlora\_Abblnd.

DR Pfam: PF00504; Chloroa\_b-bind; 1.

SQ SEQUENCE 175 AA; 18747 MW; 2EE8E8B33614851 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 175;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 DVFAFGG 215

DB 51 DVFAFGG 57

## RESULT 50

ID Q5B6G2\_EMENI PRELIMINARY; PRT; 176 AA.

AC Q5B6G2;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Hypothetical protein.

GN ORFNames=AN0468.2.

OS Aspergillus nidulans FGSC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiiales; Trichocomaceae; Emmentella.

NCBI\_TaxId=227321;

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=FGSC A4;

RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,

RA Boughalter B., Butler J., Calvo S.E., Camarata J., Chang J.,

RA Choepel Y., Collymore A., Cook A., Cooke P., Conum B., Dearellano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Ekins T., Engels R.,

RA Erickson J., Faro S., Ferreira P., Fitzgerald N., Gage D., Galagan J.,

RA Gardyna S., Gierke S., Graham L., Grand-Pierre N., Hafez N.,

RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,

RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,

RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,

RA Matthews C., Maudslott B., McCarthy M., Melidze J., Menes L.,

RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,

RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,

RA Oliver J., Peterson K., Phunhthang P., Pierre N., Purcell S.,

RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,

RA Roman U., Schauer S., Schupack R., Seaman S., Severy P., Shtrom S.,

RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,

RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,

RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

RA Zander E.,

RT "Genome Sequence of Aspergillus nidulans.";

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AACD01000007; EAA6567.1; -, Genomic DNA.

KM Hypothetical protein.

SQ SEQUENCE 176 AA; 18926 MW; 98BC9B122419DEA3 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GDLTGL 89

DB 169 GDLTGL 175

Search completed: January 18, 2006, 20:49:10

Job time: 83 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 20:43:47 : Search time 76 Seconds  
(without alignments)  
1358.605 Million cell updates/sec

Title: US-09-930-125-2\_COPY\_975\_1209

Perfect score: 235  
Sequence: 1 EFSRRAADPQRFVIGNEDL.....AVENPEYLPGGAAPQHP 235

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 244363 seqs, 439378781 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1763552

Minimum DB seq length: 0  
Maximum DB seq length: 235

Post-processing: Listing first 200 summaries

Database:

A\_Geneseq\_21:\*

- 1: geneseqp19808:\*
- 2: geneseqp19808:\*
- 3: geneseqp20008:\*
- 4: geneseqp20018:\*
- 5: geneseqp20028:\*
- 6: geneseqp20038:\*
- 7: geneseqp20038:\*
- 8: geneseqp20048:\*
- 9: geneseqp20058:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	75.7	224	7	ABR82073
2	168	71.5	214	8	ADP80499
3	132	56.2	217	4	AAE13121
4	84	35.7	88	8	ABO55591
5	65	27.7	162	8	ADT50881
6	65	27.7	164	8	ADT50880
7	59	25.1	59	3	AAE21202
8	59	25.1	59	5	AAE51147
9	39	16.6	135	3	AAE43787
10	38	16.2	103	9	ADY30516
11	37	15.7	221	7	ABR82070
12	37	15.7	221	7	ABR82070
13	37	15.7	221	7	ABR82070
14	37	15.7	221	7	ABR82070
15	37	15.7	221	7	ABR82070
16	37	15.7	221	7	ABR82070
17	37	15.7	221	7	ABR82070
18	37	15.7	221	7	ABR82070
19	37	15.7	221	7	ABR82070
20	37	15.7	221	7	ABR82070
21	37	15.7	221	7	ABR82070
22	37	15.7	221	7	ABR82070
23	37	15.7	221	7	ABR82070
24	37	15.7	221	7	ABR82070

25	15	6.4	15	4	AAE89108	AAE89108	HER2/neu
26	15	6.4	15	4	AAE88326	AAE88326	HER2/neu
27	15	6.4	15	4	AAE88362	AAE88362	HER2/neu
28	15	6.4	15	4	AAE89099	AAE89099	HER2/neu
29	15	6.4	15	4	AAE88294	AAE88294	HER2/neu
30	15	6.4	15	4	AAE88474	AAE88474	HER2/neu
31	15	6.4	15	4	AAE88720	AAE88720	HER2/neu
32	15	6.4	15	4	AAE89046	AAE89046	HER2/neu
33	15	6.4	15	4	AAE88360	AAE88360	HER2/neu
34	15	6.4	15	4	AAE88518	AAE88518	HER2/neu
35	15	6.4	15	4	AAE88590	AAE88590	HER2/neu
36	15	6.4	15	4	AAE88514	AAE88514	HER2/neu
37	15	6.4	15	4	AAE88540	AAE88540	HER2/neu
38	15	6.4	15	4	AAE88558	AAE88558	HER2/neu
39	15	6.4	15	4	AAE88672	AAE88672	HER2/neu
40	15	6.4	15	4	AAE88684	AAE88684	HER2/neu
41	15	6.4	15	4	AAE88566	AAE88566	HER2/neu
42	15	6.4	15	4	AAE88682	AAE88682	HER2/neu
43	15	6.4	15	4	AAE88336	AAE88336	HER2/neu
44	15	6.4	15	4	AAE89045	AAE89045	HER2/neu
45	15	6.4	15	4	AAE89109	AAE89109	HER2/neu
46	15	6.4	15	4	AAE89100	AAE89100	HER2/neu
47	15	6.4	15	4	AAE89101	AAE89101	HER2/neu
48	15	6.4	15	4	AAE89105	AAE89105	HER2/neu
49	15	6.4	15	4	AAE88346	AAE88346	HER2/neu
50	15	6.4	15	4	AAE89104	AAE89104	HER2/neu
51	15	6.4	15	4	AAE88330	AAE88330	HER2/neu
52	15	6.4	15	4	AAE88436	AAE88436	HER2/neu
53	15	6.4	15	4	AAE88700	AAE88700	HER2/neu
54	15	6.4	15	4	AAE88718	AAE88718	HER2/neu
55	15	6.4	15	4	AAE89103	AAE89103	HER2/neu
56	15	6.4	15	4	AAE89107	AAE89107	HER2/neu
57	15	6.4	15	4	AAE88476	AAE88476	HER2/neu
58	15	6.4	15	4	AAE88666	AAE88666	HER2/neu
59	15	6.4	15	4	AAE88714	AAE88714	HER2/neu
60	15	6.4	15	4	AAE88570	AAE88570	HER2/neu
61	15	6.4	15	4	AAE88614	AAE88614	HER2/neu
62	15	6.4	15	4	AAE89106	AAE89106	HER2/neu
63	15	6.4	15	4	AAE88696	AAE88696	HER2/neu
64	15	6.4	15	4	AAE88738	AAE88738	HER2/neu
65	15	6.4	15	4	AAE89044	AAE89044	HER2/neu
66	15	6.4	15	4	AAE88348	AAE88348	HER2/neu
67	15	6.4	15	4	AAE88388	AAE88388	HER2/neu
68	15	6.4	15	4	AAE89102	AAE89102	HER2/neu
69	15	6.4	15	7	ADN23119	ADN23119	Breast ca
70	15	6.4	15	8	ADN12610	ADN12610	MHC class
71	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
72	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
73	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
74	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
75	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
76	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
77	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
78	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
79	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
80	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
81	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
82	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
83	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
84	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
85	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
86	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
87	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
88	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
89	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
90	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
91	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
92	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
93	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
94	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
95	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
96	15	6.4	15	8	ADN65253	ADN65253	HER2/neu
97	15	6.4	15	8	ADN65253	ADN65253	HER2/neu

98	11	4.7	11	8	ADN64668	Adn64668 HLA bindi
99	11	4.7	11	8	ADN64670	Adn64670 HLA bindi
100	11	4.7	11	8	ADN64666	Adn64666 HLA bindi
101	11	4.7	11	8	ADN64664	Adn64664 HLA bindi
102	11	4.7	11	8	ADP80282	Adp80282 Human HLA
103	11	4.7	11	8	ADP79883	Adp79883 Human HLA
104	11	4.7	11	8	ADP80241	Adp80241 Human HLA
105	11	4.7	11	8	ADP80238	Adp80238 Human HLA
106	11	4.7	11	8	ADP80244	Adp80244 Human HLA
107	11	4.7	11	8	ADP80213	Adp80213 Human HLA
108	11	4.7	11	8	ADP80283	Adp80283 Human HLA
109	11	4.7	11	8	ADP80284	Adp80284 Human HLA
110	11	4.7	11	8	ADP80314	Adp80314 Human HLA
111	11	4.7	13	2	AAK52907	AAK52907 TK-SH2 as
112	11	4.7	19	2	AAW05684	AAW05684 Peptide f
113	11	4.7	21	2	AAW05683	AAW05683 Peptide f
114	10	4.3	10	2	AAK61640	AAK61640 Peptide f
115	10	4.3	10	2	AAK61641	AAK61641 Peptide f
116	10	4.3	10	2	AAK61541	AAK61541 Peptide f
117	10	4.3	10	2	AAK61552	AAK61552 Peptide f
118	10	4.3	10	2	AAK61601	AAK61601 Peptide f
119	10	4.3	10	2	AAK61639	AAK61639 Peptide f
120	10	4.3	10	2	AAK61638	AAK61638 Peptide f
121	10	4.3	10	2	AAK61642	AAK61642 Peptide f
122	10	4.3	10	2	AAK37962	AAK37962 Human CBR
123	10	4.3	10	2	AAK46040	AAK46040 Immunogen
124	10	4.3	10	2	AAK46513	AAK46513 Immunogen
125	10	4.3	10	2	AAK46041	AAK46041 Immunogen
126	10	4.3	10	2	AAK46437	AAK46437 Immunogen
127	10	4.3	10	2	AAK45532	AAK45532 Immunogen
128	10	4.3	10	2	AAK46514	AAK46514 Immunogen
129	10	4.3	10	2	AAK48152	AAK48152 Immunogen
130	10	4.3	10	2	AAK46438	AAK46438 Immunogen
131	10	4.3	10	2	AAK48155	AAK48155 Immunogen
132	10	4.3	10	2	AAK45993	AAK45993 Immunogen
133	10	4.3	10	2	AAK46505	AAK46505 Immunogen
134	10	4.3	10	2	AAK46389	AAK46389 Immunogen
135	10	4.3	10	4	AAK88840	AAK88840 HER2/neu
136	10	4.3	10	4	AAK27161	AAK27161 Human Leu
137	10	4.3	10	4	AAK26851	AAK26851 Human Leu
138	10	4.3	10	4	AAK97586	AAK97586 Human com
139	10	4.3	10	5	AAK20480	AAK20480 Naturally
140	10	4.3	10	5	ABG68433	ABG68433 Erb2 site
141	10	4.3	10	5	AAU77115	AAU77115 Human Her
142	10	4.3	10	5	ABJ00198	ABJ00198 Her2/neu
143	10	4.3	10	6	ABO01063	ABO01063 B7-1like s
144	10	4.3	10	7	ABO07288	ABO07288 Cytotoxic
145	10	4.3	10	7	ABO07316	ABO07316 CTL-sitmu
146	10	4.3	10	7	ABM00300	ABM00300 HER-2:108
147	10	4.3	10	7	ABM00328	ABM00328 Tumour-as
148	10	4.3	10	7	ADG38656	ADG38656 Human Her
149	10	4.3	10	8	ADG87869	ADG87869 Immunogen
150	10	4.3	10	8	ADG87871	ADG87871 Immunogen
151	10	4.3	10	8	ADG87832	ADG87832 Immunogen
152	10	4.3	10	8	ADG87873	ADG87873 Immunogen
153	10	4.3	10	8	ADG87783	ADG87783 Immunogen
154	10	4.3	10	8	ADG87870	ADG87870 Immunogen
155	10	4.3	10	8	ADG87772	ADG87772 Immunogen
156	10	4.3	10	8	ADG87872	ADG87872 Immunogen
157	10	4.3	10	8	ADN64634	ADN64634 HLA bindi
158	10	4.3	10	8	ADN64632	ADN64632 HLA bindi
159	10	4.3	10	8	ADN64633	ADN64633 HLA bindi
160	10	4.3	10	8	ADN64637	ADN64637 HLA bindi
161	10	4.3	10	8	ADN64635	ADN64635 HLA bindi
162	10	4.3	10	8	ADN64636	ADN64636 HLA bindi
163	10	4.3	10	8	ADP79943	ADP79943 Human HLA
164	10	4.3	10	8	ADP80190	ADP80190 Human HLA
165	10	4.3	10	8	ADP80240	ADP80240 Human HLA
166	10	4.3	10	8	ADP80338	ADP80338 Human HLA
167	10	4.3	10	8	ADP80281	ADP80281 Human HLA
168	10	4.3	10	8	ADP80339	ADP80339 Human HLA
169	10	4.3	10	8	ADP80310	ADP80310 Human HLA
170	10	4.3	10	8	ADP79821	ADP79821 Human HLA
171	10	4.3	10	8	ADP80341	ADP80341 Human HLA
172	10	4.3	10	8	ADP80189	ADP80189 Human HLA
173	10	4.3	10	8	ADP79939	ADP79939 Human HLA
174	10	4.3	10	8	ADP80188	ADP80188 Human HLA
175	10	4.3	10	4	AAK88903	AAK88903 HER2/neu
176	10	4.3	10	4	AAK88909	AAK88909 HER2/neu
177	10	4.3	10	4	AAK88917	AAK88917 HER2/neu
178	10	4.3	10	4	AAK26876	AAK26876 Human Leu
179	10	4.3	10	4	AAU26878	AAU26878 Human Leu
180	10	4.3	10	4	AAU26924	AAU26924 Human Leu
181	10	4.3	10	4	AAU26925	AAU26925 Human Leu
182	10	4.3	10	4	AAK76218	AAK76218 Tumour as
183	10	4.3	10	4	AAK76220	AAK76220 Tumour as
184	10	4.3	10	4	AAK76222	AAK76222 Tumour as
185	10	4.3	10	4	AAK76217	AAK76217 Tumour as
186	10	4.3	10	7	ADM32836	ADM32836 HLA bindi
187	10	4.3	10	7	ADM32839	ADM32839 HLA bindi
188	10	4.3	10	8	ADP79884	ADP79884 Human HLA
189	10	4.3	10	8	ABO07312	ABO07312 Human HER
190	10	4.3	10	7	ABM00324	ABM00324 HER-2 B69
191	10	4.3	10	8	AAK98966	AAK98966 HLA class
192	10	4.3	10	8	ADM12613	ADM12613 MHC class
193	10	4.3	10	8	ADK38844	ADK38844 Human Her
194	10	4.3	10	8	ADM88102	ADM88102 Human HER
195	10	4.3	10	9	AAK98976	AAK98976 HLA class
196	10	4.3	10	3	AAK89110	AAK89110 HER2/neu
197	10	4.3	10	4	AAK88750	AAK88750 HER2/NEU
198	10	4.3	10	4	AAK78834	AAK78834 c-ErbB2 (
199	10	4.3	10	2	AAK59238	AAK59238 Peptide f
200	9	3.8	9	2	AAK59238	AAK59238 Peptide f

## ALIGNMENTS

RESULT 1  
ABR82073  
ABR82073 standard; protein; 224 AA.

ID ABR82073; (first entry)  
AC ABR82073; (first entry)  
XX 23-SEP-2003 (first entry)  
XX Distal human Her2/neu amino acid sequence SEQ ID NO:13.

DE Human; Her2/neu; Her2/neu target antigen; immune response; cytostatic;  
XX Human; Her2/neu; Her2/neu target antigen; immune response; cytostatic;  
XX immunostimulant; vaccine; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers  
XX Misc-difference 3 /note= "encoded by GAGC"

FT Misc-difference 139 /note= "encoded by GCC"  
FT Misc-difference 139 /note= "encoded by GCC"

XX WO2003055439-A2.

XX 10-JUL-2003.

XX 18-JUL-2002; 2002MO-US022975.

XX 18-JUL-2001; 2001US-0306250P.

XX (REGC ) UNIV CALIFORNIA.

XX Nelson EL;

XX WPI; 2003-569400/53.

XX N-PSDB; ACF06079.

XX New Her2/neu target antigens and polynucleotides encoding them, useful  
PT for stimulating immunoeffector cells or an immune response in a subject



PT against cancer cells expressing Her2/neu, and for vaccination strategies.  
XX  
XX Example 1; Fig 7B; 83pp; English.  
XX  
XX The present invention describes a recombinant polynucleotide (I)  
CC comprising a first nucleotide sequence encoding a Her2/neu target antigen  
CC consisting of an amino acid sequence corresponding to: (a) amino acid  
CC residues 634-663 or 606-683 operatively linked to amino acid residues  
CC 1035-1255 of human Her2/neu (SEQ ID NO:1, ABR82066); or (b) amino acid  
CC residues 635-685 or 608-685 operatively linked to amino acid residues  
CC 1037-1257 of rat Her2/neu (SEQ ID NO:2, ABR82067). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. The  
CC polynucleotide encoding a Her2/neu target antigen can be used for  
CC stimulating immunoeffector cells or an immune response in a subject  
CC against cancer cells expressing Her2/neu. The encoded Her2/neu target  
CC antigen polypeptide is useful as a tag to detect or isolate the fusion  
CC protein containing the Her2/neu target an immune response stimulated by  
CC the Her2/neu target antigen. The Her2/neu target antigen polynucleotides  
CC and polypeptides are useful in genetic or polypeptide vaccination  
CC strategies. The present sequence represents distal human Her2/neu, which  
CC is used in the exemplification of the present invention  
XX  
SQ Sequence 224 AA;  
Query Match 75.7%; Score 178; DB 7; Length 224;  
Best Local Similarity 100.0%; Pred. No. 8.5e-157; Indels 0; Gaps 0;  
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 58 CPDPAPAGAGMVMHRRSSSTRSGGDLTLGLEPSEBEAPRSLAPSEAGSDVFPDGLG 117  
DB 1 CPDPAPAGAGMVMHRRSSSTRSGGDLTLGLEPSEBEAPRSLAPSEAGSDVFPDGLG 60  
QY 118 MGAAGLQSLPTHTDPSPLQRYSEDPVPLPSETDGYVAPLTGSPQPEYVNOQPVRRQPPS 177  
DB 61 MGAAGLQSLPTHTDPSPLQRYSEDPVPLPSETDGYVAPLTGSPQPEYVNOQPVRRQPPS 120  
QY 178 PRGGPLPAARPAATLERPKTLSPGKNGVVKDVFARFGAVENPEYLTPOGGAAPQPHP 235  
DB 121 PRGGPLPAARPAATLERPKTLSPGKNGVVKDVFARFGAVENPEYLTPOGGAAPQPHP 178  
RESULT 2  
ADP80499 standard; protein; 214 AA.  
XX  
XX ADP80499;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX Human epitope vaccine-related Her2/neu protein SeqID758.  
XX  
XX epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44;  
XX tumour associated antigen peptide; cytostatic; vaccine; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2004052917-A2.  
XX  
XX 24-JUN-2004.  
XX  
XX 10-DEC-2003; 2003WO-US038949.  
XX  
XX 10-DEC-2002; 2002US-0432017P.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Keogh EA, Southwood S, Fikes JD, Sette A;  
XX  
XX WPI, 2004-468809/44.  
XX  
XX New HLA-A1, A2, A3, A24, B7 or B44 tumor associated antigen peptides,  
XX useful in preparing a composition for diagnosing or treating tumor  
XX associated antigen-related disease.  
PT

XX  
XX Disclosure; SEQ ID NO 758; 244pp; English.  
XX  
XX This invention relates to a novel isolated peptide which comprises at  
CC least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given  
CC in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or  
CC B44 tumor associated antigen peptide. The invention may be useful for  
CC the production of compounds with a cytostatic activity or for the  
CC production of a vaccine. The peptide is useful in preparing a composition  
CC diagnosing or treating tumor associated antigen-related disease. The  
CC present sequence is that of a protein which may be used to derive epitope  
CC peptides for use in the peptide of the invention.  
XX  
SQ Sequence 214 AA;  
Query Match 71.5%; Score 168; DB 8; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.6e-147; Indels 0; Gaps 0;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 MYHHRSSSTRSGGDLTLGLEPSEBEAPRSLAPSEAGSDVFPDGLGMGAAGLQSL 127  
DB 1 MYHHRSSSTRSGGDLTLGLEPSEBEAPRSLAPSEAGSDVFPDGLGMGAAGLQSL 60  
QY 128 PTHDPSPLQRYSEDPVPLPSETDGYVAPLTGSPQPEYVNOQPVRRQPPSPREGPLPAAR 187  
DB 61 PTHDPSPLQRYSEDPVPLPSETDGYVAPLTGSPQPEYVNOQPVRRQPPSPREGPLPAAR 120  
QY 188 PAGATLERPKTLSPGKNGVVKDVFARFGAVENPEYLTPOGGAAPQPHP 235  
DB 121 PAGATLERPKTLSPGKNGVVKDVFARFGAVENPEYLTPOGGAAPQPHP 168  
RESULT 3  
AAE13121  
ID AAE13121 standard; protein; 217 AA.  
XX  
XX AAE13121;  
XX  
XX 28-JAN-2002 (first entry)  
XX  
XX Mature human HER-2 membrane distal intracellular domain.  
XX  
XX Immunostimulatory fusion protein; IFP; antigen component; therapy;  
XX immunostimulatory component; T-cell mediated immune response; DC;  
XX dendritic cell; colon cancer; breast carcinoma; ovarian cancer; human;  
XX HER-2 membrane distal intracellular domain.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX PN WO200174855-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US010515.  
XX  
XX 30-MAR-2000; 2000US-0193504P.  
XX  
XX (DENB-) DENDREON CORP.  
XX  
XX Laus R, Vidovic D, Graddie T;  
XX  
XX WPI; 2001-662965/76.  
XX  
XX DR N-PSDB; AAD21572.  
XX  
XX An immunostimulatory fusion protein comprising the intracellular domain  
XX of HER-2 and an antigen elicits an immune response to the antigen and is  
XX useful for the treatment of associated cancer associated.  
XX  
XX Claim 2; Page 31; 59pp; English.  
XX  
XX The invention relates to immunostimulatory fusion proteins (IFP) and  
XX nucleic acid molecules encoding such proteins. The IFPs comprise a  
XX polypeptide antigen component and an immunostimulatory component derived  
CC

CC from the intracellular domain of HER-2 protein which is effective to  
CC elicit a protective dendritic cell (DC)-induced T-cell mediated cellular  
CC immune response to the antigen. TTP or superactivated dendritic cells are  
CC used to treat cancer e.g. breast carcinoma, ovarian and colon cancer  
CC associated with a particularly antigen. The present sequence is mature  
CC human HER-2 membrane distal intracellular domain. This sequence is used  
CC in the HER500 and HER300 GM-CSF fusion constructs of the invention  
XX  
SQ Sequence 217 AA;  
  
Query Match 56.2%; Score 132; DB 4; Length 217;  
Best Local Similarity 100.0%; Pred. No. 4.8e-114;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 64 GAGGVNHRHRSSTRSGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKG 123  
DB 1 GAGGVNHRHRSSTRSGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKG 60  
DB 124 LQSLPTHDPSPLOQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNPDPVAPQPPSPREGPL 183  
61 LQSLPTHDPSPLOQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNPDPVAPQPPSPREGPL 120  
QY 184 PAARPAATLER 195  
DB 121 PAARPAATLER 132  
  
RESULT 4  
ABO55591  
ID ABO55591 standard; protein; 88 AA.  
AC ABO55591;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human genome derived single exon protein #1825.  
XX  
KW Human; gene expression; single exon probe; microarray;  
XX alternative splicing event; genomic alteration.  
XX  
OS Homo sapiens.  
XX  
PN US2003194704-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 03-APR-2002; 2002US-00029386.  
XX  
PR 03-APR-2002; 2002US-00029386.  
XX  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
XX  
PI Penn SG, Rank DR, Hanzel DK;  
XX  
DR WPI; 2004-119264/12.  
XX  
PT New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.  
XX  
PS Claim 45; SEQ ID NO 29225; 80pp; English.  
XX  
XX The invention relates to a nucleic acid probe for measuring human gene  
XX expression, comprising any of the 27,400 fully defined nucleotide  
XX sequences in the specification, or their complements or fragments, and  
XX encoding at least 8 amino acids of any of the 688 amino acid sequences  
XX fully defined in the specification. The probe is a single exon probe that  
XX hybridises under high stringency conditions to a nucleic acid molecule  
XX expressed in human cells or tissues. Also included are a spatially-  
XX addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterising  
CC alternative splicing events, in detecting and characterising gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence data for  
CC single exon probe protein of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20030194704  
XX  
SQ Sequence 88 AA;  
  
Query Match 35.7%; Score 84; DB 8; Length 88;  
Best Local Similarity 100.0%; Pred. No. 8.7e-70;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 80 SGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKGSLPTHDPSPLOQRY 139  
DB 3 SGGDLTLGLPSEERAPRPLAPSGAGSDVFDGLGMAKKGSLPTHDPSPLOQRY 62  
QY 140 EDPVPLPSETDGYVAPLTCSPQ 163  
DB 63 EDPVPLPSETDGYVAPLTCSPQ 86  
  
RESULT 5  
ADT50881  
ID ADT50881 standard; protein; 162 AA.  
AC ADT50881;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Cancer related protein sequence #44.  
XX  
KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;  
KW ovarian; prostate; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004092338-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 12-APR-2004; 2004WO-US011104.  
XX  
PR 11-APR-2003; 2003US-0462399P.  
PR 01-JUL-2003; 2003US-0484333P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Macina RA, Turner LR, Sun Y, Tam A;  
XX  
DR WPI; 2004-766851/75.  
XX



## RESULT 8

AA051147  
ID AA051147 standard; protein; 59 AA.  
XX  
AC AA051147;  
XX  
DT 17-JUN-2002 (first entry)  
XX  
DE Human Her-2/neu oncoprotein phosphorylation domain fragment.  
XX  
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200212341-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 03-AUG-2001; 2001WO-US024283.  
XX  
PR 03-AUG-2000; 2000US-00632507.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Cheever MA, Cheyssen D;  
XX  
DR WPI; 2002-241743/29.  
XX  
PT Her-2/neu fusion protein for treating or preventing cancer by eliciting  
PT or enhancing an immune response to the protein, has Her-2/neu  
PT extracellular domain fused to Her-2/neu intracellular or phosphorylation  
PT domain.  
XX  
PS Disclosure; Fig 11; 141pp; English.  
XX  
CC The present sequence is that of a fragment (Deltap) of the  
CC phosphorylation domain of human Her-2/neu (p185 glycoprotein, c-erbB2),  
CC an oncogenic self-protein and target for anti-cancer vaccines. The Her-  
CC 2/neu gene is amplified and p185 is overexpressed in breast, ovarian,  
CC colon, lung and prostate cancer. Her-2/neu (see AA051143) is a member of  
CC the tyrosine kinase family of receptor-like glycoproteins. It comprises  
CC an extracellular domain with homology to the epidermal growth factor  
CC receptor (EGFR), a highly hydrophobic transmembrane domain and a C-  
CC terminal intracellular domain that also shows homology to EGFR. Its  
CC overexpression correlates with a poor prognosis in breast and ovarian  
CC cancers. The invention provides Her-2/neu fusion proteins, nucleic acids  
CC encoding them, viral vectors, and vaccines comprising the fusion proteins  
CC or nucleic acid molecules. In preferred fusion proteins, the  
CC extracellular domain of a Her-2/neu protein is fused to a Her-2/neu  
CC intracellular domain or phosphorylation domain (or the Deltap fragment).  
CC An immune response to Her-2/neu protein is elicited or enhanced by  
CC administering the fusion protein in the form of a vaccine, or by  
CC transfecting cells of an animal *ex vivo* with a nucleic acid encoding the  
CC fusion protein, and delivering the transfected cells to the animal. The  
CC fusion proteins, nucleic acids, and isolated specific T-cells are useful  
CC for inhibiting the development of a cancer, especially breast, ovarian,  
CC colon, lung or prostate cancer in a patient. T cells that specifically  
CC react with a Her-2/neu fusion protein can be used to remove tumour cells  
CC from a sample in order to inhibit the development of cancer in a patient  
XX  
SQ Sequence 59 AA;

Query Match 25.1%; Score 59; DB 5; Length 59;  
Best Local Similarity 100.0%; Pred. No. 1e-46;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QNEDIGPASPPLDSTFYRSLLEDMDGLVDAERYLVPOGFCPPDPAAGAGVHRRHR 74  
DB 1 QNEDIGPASPPLDSTFYRSLLEDMDGLVDAERYLVPOGFCPPDPAAGAGVHRRHR 59

## RESULT 9

AA043787  
ID AA043787 standard; protein; 135 AA.  
XX  
AC AA043787;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated protein sequence SEQ ID NO:1222.  
XX  
KW Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
KW antidiabetic; antiaesthetic; antirheumatic; antichrystic; antiviral;  
KW antiinflammatory; antichryd; antiallergic; antibacterial; cardiant;  
KW dermatologic; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
XX  
OS Homo sapiens.  
XX  
PN WO200055350-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005882.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-587533/55.  
XX  
DR N-PSDB; AAC77996.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
PT useful for treating or diagnosing e.g. cancer.  
XX  
PS Claim 11; Page 1864; 2352pp; English.  
XX  
CC AAC7607 to AAC7848 encode the human cancer associated proteins given in  
CC AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnery; immunomodulator;  
CC antidiabetic; antiaesthetic; antirheumatic; antichrystic;  
CC antiinflammatory; antichryd; antiallergic; antibacterial; antiviral;  
CC dermatologic; neuroprotective; cardiant; thrombolytic; coagulant;  
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC7849 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 135 AA;

Query Match 16.6%; Score 39; DB 3; Length 135;  
Best Local Similarity 100.0%; Pred. No. 8.9e-26;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      197 KTLSFGKNGVVKDVPFAGGAVENPEYLTPOGGAAPQHP 235
DB      51 KTLSFGKNGVVKDVPFAGGAVENPEYLTPOGGAAPQHP 89

RESULT 10
ID      ADY30516 standard; protein; 103 AA.
AC      ADY30516;
AD      ADY30516;
XX      05-MAY-2005 (first entry)
XX      Human splice variant protein expressed in ovary cells DEX0487_002.aa.5.
XX      ovarian tumor; diagnosis; prognosis; vaccine; cytostatic; gene therapy.
XX      Homo sapiens.
XX      MO2005017102-A2.
XX      24-FEB-2005.
XX      01-JUN-2004; 2004MO-US017156.
XX      30-MAY-2003; 2003US-0474856P.
XX      (DIAD-) DIADEXUS INC.
XX      Macina RA, Turner LR, Sun Y;
XX      WPI; 2005-182347/19.
XX      N-PSDB; ADY30412.
XX      New ovarian specific nucleic acid (OSNA) molecules and polypeptides,
XX      useful for diagnosing, monitoring or treating, and detecting the presence
XX      of, ovarian cancer in a subject.
XX      Claim 12; SEQ ID NO 111; 834bp; English.
XX      This invention relates to novel isolated nucleic acid molecules and the
XX      encoding polypeptides thereof that are present in normal and neoplastic
XX      ovarian cells. Specifically, it refers to splice variants of these
XX      polynucleotides. The present invention describes generating antibodies,
XX      as well as agonists and antagonists of the polypeptides that can be used
XX      in the diagnosis, monitoring, staging, imaging and treatment of ovarian
XX      cancer and non-cancerous disease states of the ovary. Furthermore, it
XX      provides a kit for detecting the risk of cancer or the presence of cancer
XX      in patient that comprises a means for determining the presence of a
XX      nucleic acid or protein as given in the specification. These nucleic acid
XX      and protein molecules can also be used to induce an immune response and
XX      hence be useful in the development of a vaccine for the treatment of
XX      ovarian cancer. Accordingly, compositions derived thereof exhibit
XX      cytostatic activity and can be used for gene therapy purposes. This
XX      polypeptide is encoded by a human splice variant DNA sequence that is
XX      expressed in ovarian cells, given in an exemplification of the invention.
XX      Sequence 103 AA;

Query Match      16.2%; Score 38; DB 9; Length 103;
Best Local Similarity 100.0%; Pred. No. 5,8e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      198 TLSFGKNGVVKDVPFAGGAVENPEYLTPOGGAAPQHP 235
DB      20 TLSFGKNGVVKDVPFAGGAVENPEYLTPOGGAAPQHP 57

RESULT 11
ID      ABR82070 standard; protein; 221 AA.
AC      ABR82070;
XX      ABR82070;

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XX      23-SEP-2003 (first entry)
XX      Terminal rat Her2/neu amino acid sequence SEQ ID NO:7.
XX      Rat; Her2/neu; Her2/neu target antigen; immune response; cytostatic;
XX      immunostimulant; vaccine; cancer.
XX      Rattus norvegicus.
XX      MO2003055439-A2.
XX      10-JUL-2003.
XX      18-JUL-2002; 2002MO-US022975.
XX      18-JUL-2001; 2001US-0306250P.
XX      (REGC ) UNIV CALIFORNIA.
XX      Nelson BL;
XX      WPI; 2003-569400/53.
XX      N-PSDB; ACF06076.
XX      New Her2/neu target antigens and polynucleotides encoding them, useful
XX      for stimulating immunoeffector cells or an immune response in a subject
XX      against cancer cells expressing Her2/neu, and for vaccination strategies.
XX      Example 1; Fig 6B; 83bp; English.
XX      The present invention describes a recombinant polynucleotide (I)
XX      comprising a first nucleotide sequence encoding a Her2/neu target antigen
XX      consisting of an amino acid sequence corresponding to: (a) amino acid
XX      residues 634-683 or 606-683 operatively linked to amino acid residues
XX      1035-1255 of human Her2/neu (SEQ ID NO:1; ABR82066); or (b) amino acid
XX      residues 635-685 or 608-685 operatively linked to amino acid residues
XX      1037-1257 of rat Her2/neu (SEQ ID NO:2; ABR82067). (I) has cytostatic and
XX      immunostimulant activities, and can be used in vaccines. The
XX      polynucleotide encoding a Her2/neu target antigen can be used for
XX      stimulating immunoeffector cells or an immune response in a subject
XX      against cancer cells expressing Her2/neu. The encoded Her2/neu target
XX      antigen polypeptide is useful as a tag to detect or isolate the fusion
XX      protein containing the Her2/neu target an immune response stimulated by
XX      the Her2/neu target antigen. The Her2/neu target antigen polynucleotides
XX      and polypeptides are useful in genetic or polypeptide vaccination
XX      strategies. The present sequence represents terminal rat Her2/neu, which
XX      is used in the exemplification of the present invention
XX      Sequence 221 AA;

Query Match      15.7%; Score 37; DB 7; Length 221;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      187 RPAQATLERPKTSLSPGKNGVVKDVPFAGGAVENPEYL 223
DB      127 RPAQATLERPKTSLSPGKNGVVKDVPFAGGAVENPEYL 163

RESULT 12
ID      AAY98969 standard; peptide; 15 AA.
AC      AAY98969;
AD      AAY98969;
XX      07-AUG-2000 (first entry)
XX      HLA class II binding antigen epitope peptide #158.
XX      Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
XX      immune response; chronic viral disease; cancer; autoimmune disease;
XX      rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;

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KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
XX  
XX WO961916-A1.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Sette A, Southwood S, Sidney J;  
XX  
XX WPI; 2000-097143/08.  
XX  
XX  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX  
XX  
XX Claim 1; Page 42; 60pp; English.  
XX  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
XX helper T cell response. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 41 GDLVDAEYLVPOQG 55  
DB 1 GDLVDAEYLVPOQG 15  
RESULT 13  
AAY98875  
ID AAY98875 standard; peptide; 15 AA.  
XX  
XX AAY98875;  
AC  
XX 07-AUG-2000 (first entry)  
DT  
XX  
XX HLA class II binding antigen epitope peptide #64.  
, DE

XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
XX immune response; chronic viral disease; cancer; autoimmune disease;  
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
XX  
XX WO961916-A1.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
XX Sette A, Southwood S, Sidney J;  
XX  
XX WPI; 2000-097143/08.  
XX  
XX  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX  
XX  
XX Claim 1; Page 41; 60pp; English.  
XX  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
XX helper T cell response. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 150 TDGYVAPLTCSPQPE 164  
DB 1 TDGYVAPLTCSPQPE 15  
RESULT 14  
AAY98965  
ID AAY98965 standard; peptide; 15 AA.  
XX  
XX AAY98965;  
AC

XX 07-AUG-2000 (first entry)  
XX HLA class II binding antigen epitope peptide #154.  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
XX immune response; chronic viral disease; cancer; autoimmune disease;  
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
XX allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
XX glomerulonephritis; food hypersensitivity; malaria.  
XX Unidentified.  
XX WO9961916-A1.  
XX 02-DEC-1999.  
XX 28-MAY-1999; 99WO-US012066.  
XX 29-MAY-1998; 98US-0087192P.  
XX (EPIM-) EPIMMUNE INC.  
XX Sette A, Southwood S, Sidney J;  
XX WPI, 2000-097143/08.  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX Claim 1; Page 42; 60pp; English.  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical focuses the immune response  
XX helper T cell response. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX Sequence 15 AA;  
XX  
XX Query Match 6.4%; Score 15; DB 3; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 2 FSRMARDPQRFVVIQ 16  
XX 1 FSRMARDPQRFVVIQ 15  
XX  
XX RESULT 15

AAV98970  
ID AAV98970 standard; peptide; 15 AA.  
XX AAV98970;  
XX 07-AUG-2000 (first entry)  
XX HLA class II binding antigen epitope peptide #159.  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
XX immune response; chronic viral disease; cancer; autoimmune disease;  
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
XX allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
XX glomerulonephritis; food hypersensitivity; malaria.  
XX Unidentified.  
XX WO9961916-A1.  
XX 02-DEC-1999.  
XX 28-MAY-1999; 99WO-US012066.  
XX 29-MAY-1998; 98US-0087192P.  
XX (EPIM-) EPIMMUNE INC.  
XX Sette A, Southwood S, Sidney J;  
XX WPI, 2000-097143/08.  
XX New compositions containing immunogenic peptide epitopes for various HLA  
XX class II DR molecules useful for inducing helper T cell response.  
XX Claim 1; Page 42; 60pp; English.  
XX The present invention relates to a new pharmaceutical composition  
XX comprising a unit dose form of a peptide, or analogue, comprising an  
XX epitope selected from those represented by peptides AAY98812-Y99339 which  
XX are derived from various antigens for various human leucocyte antigen  
XX class DR molecules, representative of the world wide population. The  
XX peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
XX than or equal to 1,000 nM. The pharmaceutical focuses the immune response  
XX helper T cell response. The pharmaceutical focuses the immune response  
XX towards selected determinants and could therefore be used in cases of  
XX chronic viral diseases and cancer. Examples of diseases that can be  
XX treated using the peptide containing pharmaceutical include autoimmune  
XX diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
XX gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
XX streptococcal endocarditis or glomerulonephritis and food  
XX hypersensitivities. The peptide epitopes can be used to enhance immune  
XX responses against other immunogens administered with the peptides.  
XX Diseases which can be treated using immunogenic mixtures include prostate  
XX cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
XX carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
XX used to make monoclonal antibodies useful as potential diagnostic or  
XX therapeutic agents. The peptides may also be useful as diagnostic  
XX reagents, for example, to determine the susceptibility of an individual  
XX to a treatment regimen. Also, the peptides may be used to predict which  
XX individuals will be at substantial risk of developing chronic infection.  
XX The selection of appropriate T and B cell epitopes should allow the  
XX development of epitope based vaccines particularly towards conserved  
XX epitopes of pathogens which are characterized by high sequence  
XX variability such as HIV, HCV and Malaria  
XX Sequence 15 AA;  
XX  
XX Query Match 6.4%; Score 15; DB 3; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 54 QGFPCDPAPAGGM 68  
XX  
XX RESULT 15



Db 1 QGFFCPCDPAPGAGGM 15

## RESULT 16

ID AAY98973 standard; peptide; 15 AA.

AC AAY98973;

DT 07-AUG-2000 (First entry)

DE HLA class II binding antigen epitope peptide #162.

KM Human leucocyte antigen, HLA class II; antigen epitope; pharmaceutical  
 KM immune response; chronic viral disease; cancer; autoimmune disease;  
 KM rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
 KM allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
 KM glomerulonephritis; food hypersensitivity; malaria.

OS Unidentified.

PN W09961916-A1.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US012066.

PR 29-MAY-1998; 98US-0087192P.

PA (EPIM-) EPIMUNE INC.

PI Sette A, Southwood S, Sidney J;

DR WPI; 2000-097143/08.

PT New compositions containing immunogenic peptide epitopes for various HLA  
PT class II DR molecules useful for inducing helper T cell response.

PS Claim 1; Page 42; 60pp; English.

The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides AA198812-199319 which are derived from various antigens for various human leukocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence variability such as HIV, HCV and Malaria

**SQ Sequence 15 AA;**

Query Match	6.4%;	Score 15;	DB 3;	Length 15;
Best Local Similarity	100.0%;	Pred. No.	2.3e-06;	

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 135 LQRYSEDPTVLPSE 149

Db 1 LQRYSEDPVPLPSE 15

### RESULT 17

ID AAY98975 standard; peptide; 15 AA.

AC AAY98975;

DT 07-AUG-2000 (first entry)

DE HLA class II binding antigen epitope peptide #164.

KM Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical  
KM immune response; chronic viral disease; cancer; autoimmune disease;  
KM rheumatoid arthritis; multiple sclerosis; myosinemia gravis; AIDS;  
KM allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KM glomerulonephritis; food hypersensitivity; malaria.

OS Unidentified.

PN WO9961916-A1.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US012066.

PR 29-MAY-1998; 98US-0087192P.

PA (EPIM-) EPIMUNE INC.

PI Sette A, Southwood S, Sidney J;

DR WPI; 2000-097143/08.

PT New compositions containing immunogenic peptide epitopes for various HLA  
PT class II DR molecules useful for inducing helper T cell response.

PS Claim 1; Page 42; 60pp; English.

The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides AAY98812-199339 which are derived from various antigens for various human leucocyte antigen class II molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence variability such as HIV, HCV and Malaria



SQ Sequence 15 AA;  
 Query Match 6.4%; Score 15; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 203 KNGVWQVPAFGAV 217  
 |||||  
 1 KNGVWQVPAFGAV 15  
 Db  
 RESULT 18  
 AAY98967  
 ID AAY98967 standard; peptide; 15 AA.  
 AC AAY98967;  
 DT 07-AUG-2000 (first entry)  
 XX  
 XX HLA class II binding antigen epitope peptide #156.  
 DE  
 XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
 KW immune response; chronic viral disease; cancer; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
 KW glomerulonephritis; food hypersensitivity; malaria.  
 OS Unidentified.  
 XX  
 XX MO961916-A1.  
 XX  
 XX 02-DEC-1999.  
 XX  
 XX 28-MAY-1999; 99WO-US012066.  
 XX  
 XX 29-MAY-1998; 98US-0087192P.  
 XX  
 PA (EPIIM-) EPIIMUNE INC.  
 PI Sette A, Southwood S, Sidney J;  
 XX  
 XX WPI; 2000-097143/08.  
 PT New compositions containing immunogenic peptide epitopes for various HLA  
 PT class II DR molecules useful for inducing helper T cell response.  
 XX  
 XX  
 PS Claim 1; Page 42; 60pp; English.  
 CC The present invention relates to a new pharmaceutical composition  
 CC comprising a unit dose form of a peptide, or analogue, comprising an  
 CC epitope selected from those represented by peptides AY98812-Y9939 which  
 CC are derived from various antigens for various human leucocyte antigen  
 CC class DR molecules, representative of the world wide population. The  
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
 CC helper T cell response. The pharmaceutical focuses the immune response  
 CC towards selected determinants and could therefore be used in cases of  
 CC chronic viral diseases and cancer. Examples of diseases that can be  
 CC treated using the peptide containing pharmaceutical include autoimmune  
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
 CC streptococcal endocarditis or glomerulonephritis and food  
 CC hypersensitivities. The peptide epitopes can be used to enhance immune  
 CC responses against other immunogens administered with the peptides.  
 CC Diseases which can be treated using immunogenic mixtures include prostate  
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
 CC used to make monoclonal antibodies useful as potential diagnostic or  
 CC therapeutic agents. The peptides may also be useful as diagnostic  
 CC reagents, for example, to determine the susceptibility of an individual  
 CC to a treatment regimen. Also, the peptides may be used to predict which  
 CC individuals will be at substantial risk of developing chronic infection.  
 CC The selection of appropriate T and B cell epitopes should allow the

CC development of epitope based vaccines particularly towards conserved  
 CC epitopes of pathogens which are characterized by high sequence  
 CC variability such as HIV, HCV and Malaria  
 CC  
 SQ Sequence 15 AA;  
 Query Match 6.4%; Score 15; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 31 YRSLLEDMDGLVD 45  
 |||||  
 1 YRSLLEDMDGLVD 15  
 Db  
 RESULT 19  
 AAY98972  
 ID AAY98972 standard; peptide; 15 AA.  
 AC AAY98972;  
 DT 07-AUG-2000 (first entry)  
 XX  
 XX HLA class II binding antigen epitope peptide #161.  
 DE  
 XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
 KW immune response; chronic viral disease; cancer; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
 KW glomerulonephritis; food hypersensitivity; malaria.  
 OS Unidentified.  
 XX  
 XX MO961916-A1.  
 XX  
 XX 02-DEC-1999.  
 XX  
 XX 28-MAY-1999; 99WO-US012066.  
 XX  
 XX 29-MAY-1998; 98US-0087192P.  
 XX  
 PA (EPIIM-) EPIIMUNE INC.  
 PI Sette A, Southwood S, Sidney J;  
 XX  
 XX WPI; 2000-097143/08.  
 PT New compositions containing immunogenic peptide epitopes for various HLA  
 PT class II DR molecules useful for inducing helper T cell response.  
 XX  
 XX  
 PS Claim 1; Page 42; 60pp; English.  
 CC The present invention relates to a new pharmaceutical composition  
 CC comprising a unit dose form of a peptide, or analogue, comprising an  
 CC epitope selected from those represented by peptides AY98812-Y9939 which  
 CC are derived from various antigens for various human leucocyte antigen  
 CC class DR molecules, representative of the world wide population. The  
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
 CC helper T cell response. The pharmaceutical focuses the immune response  
 CC towards selected determinants and could therefore be used in cases of  
 CC chronic viral diseases and cancer. Examples of diseases that can be  
 CC treated using the peptide containing pharmaceutical include autoimmune  
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
 CC streptococcal endocarditis or glomerulonephritis and food  
 CC hypersensitivities. The peptide epitopes can be used to enhance immune  
 CC responses against other immunogens administered with the peptides.  
 CC Diseases which can be treated using immunogenic mixtures include prostate  
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
 CC used to make monoclonal antibodies useful as potential diagnostic or  
 CC therapeutic agents. The peptides may also be useful as diagnostic

CC reagents, for example, to determine the susceptibility of an individual  
CC to a treatment regimen. Also, the peptides may be used to predict which  
CC individuals will be at substantial risk of developing chronic infection.  
CC The selection of appropriate T and B cell epitopes should allow the  
CC development of epitope based vaccines particularly towards conserved  
CC epitopes of pathogens which are characterized by high sequence  
CC variability such as HIV, HCV and Malaria  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 109 SDVFDGDLGMGAAG 123  
1 SDVFDGDLGMGAAG 15  
DB 1 SDVFDGDLGMGAAG 15  
RESULT 20  
ID AAY98874 standard; peptide; 15 AA.  
XX AAY98874;  
AC AAY98874;  
XX 07-AUG-2000 (first entry)  
DT  
XX HLA class II binding antigen epitope peptide #63.  
DE  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
KW immune response; chronic viral disease; cancer; autoimmune disease;  
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
OS  
XX WO961916-A1.  
PN  
XX 02-DEC-1999.  
PD  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
PA  
XX Sette A, Southwood S, Sidney J;  
PI  
XX WPI, 2000-097143/08.  
DR  
XX New compositions containing immunogenic peptide epitopes for various HLA  
PT class II DR molecules useful for inducing helper T cell response.  
PS  
XX Claim 1; Page 41; 60pp; English.  
XX  
XX The present invention relates to a new pharmaceutical composition  
CC comprising a unit dose form of a peptide, or analogue, comprising an  
CC epitope selected from those represented by peptides AAY98812-Y9339 which  
CC are derived from various antigens for various human leucocyte antigen  
CC class DR molecules, representative of the world wide population. The  
CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of  
CC chronic viral diseases and cancer. Examples of diseases that can be  
CC treated using the peptide containing pharmaceutical include autoimmune  
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
CC streptococcal endocarditis or glomerulonephritis and food  
CC hypersensitivities. The peptide epitopes can be used to enhance immune  
CC responses against other immunogens administered with the peptides.  
CC Diseases which can be treated using immunogenic mixtures include prostate

CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
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CC used to make monoclonal antibodies useful as potential diagnostic or  
CC therapeutic agents. The peptides may also be useful as diagnostic  
CC reagents, for example, to determine the susceptibility of an individual  
CC to a treatment regimen. Also, the peptides may be used to predict which  
CC individuals will be at substantial risk of developing chronic infection.  
CC The selection of appropriate T and B cell epitopes should allow the  
CC development of epitope based vaccines particularly towards conserved  
CC epitopes of pathogens which are characterized by high sequence  
CC variability such as HIV, HCV and Malaria  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 54 QGFPCDDPAPGAGM 68  
1 QGFPCDDPAPGAGM 15  
DB 1 QGFPCDDPAPGAGM 15  
RESULT 21  
ID AAY98971 standard; peptide; 15 AA.  
XX AAY98971;  
AC AAY98971;  
XX 07-AUG-2000 (first entry)  
DT  
XX HLA class II binding antigen epitope peptide #160.  
DE  
XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
KW immune response; chronic viral disease; cancer; autoimmune disease;  
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.  
XX  
XX Unidentified.  
OS  
XX WO961916-A1.  
PN  
XX 02-DEC-1999.  
PD  
XX 28-MAY-1999; 99WO-US012066.  
XX  
XX 29-MAY-1998; 98US-0087192P.  
XX  
XX (EPIM-) EPIMUNE INC.  
PA  
XX Sette A, Southwood S, Sidney J;  
PI  
XX WPI, 2000-097143/08.  
DR  
XX New compositions containing immunogenic peptide epitopes for various HLA  
PT class II DR molecules useful for inducing helper T cell response.  
PS  
XX Claim 1; Page 42; 60pp; English.  
XX  
XX The present invention relates to a new pharmaceutical composition  
CC comprising a unit dose form of a peptide, or analogue, comprising an  
CC epitope selected from those represented by peptides AAY98812-Y9339 which  
CC are derived from various antigens for various human leucocyte antigen  
CC class DR molecules, representative of the world wide population. The  
CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of  
CC chronic viral diseases and cancer. Examples of diseases that can be  
CC treated using the peptide containing pharmaceutical include autoimmune  
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-

streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence variability such as HIV, KCV and Malaria

chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical cancer, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved

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Query Match Similarity      6.4%; Score 15; DB 3; Length 15;
Best Local Similarity      100.0%; Pred. No. 2,3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      84 DTTGLPEPSEEDAPR 98
      |||||
db      1 DTTGLPEPSEEDAPR 15

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CC	variability such as HIV, HCV and Malaria
XX	
SO	Sequence 15 AA;
Query Match	6.4%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. NO. 2.3e-06;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0

RESULT 22  
AA98968  
ID AA98968 standard; peptide; 15 AA.

AC	AA98968;
XX	
DT	07-AUG-2000 (first entry)

HLA class II binding antigen epitope peptide #157.

KW Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical  
KW immune response; chronic viral disease; cancer; autoimmune disease;  
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;  
KW glomerulonephritis; food hypersensitivity; malaria.

OS Unidentified.

PN WO9961916-A1.

02-DEC-1999.

XX 28-MAY-1999: 99WO-US012066  
PFXX 29-MAY-1998: 98115-0087192P  
PBXX  
DA (EDTM-) EDTMINE INC

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XX New compositions containing immunogenic peptide epitopes for various HLA  
PT PT class II DR molecules useful for inducing helper T cell response.  
PT

PS Claim 1; Page 42; 60pp; English.

XX The present invention relates to a new pharmaceutical composition  
CC comprising a unit dose form of a peptide, or analogue, comprising an  
CC epitope selected from those represented by peptides AA978812-79939 which  
CC are derived from various antigens for various human leucocyte antigen  
CC class DR molecules, representative of the world wide population. The  
CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of

RESULT 23	
AA98974	
ID	AA98974 standard; peptide; 15 AA

AC AAY98974;

DT	07-AUG-2000 (first entry)
XX	
DE	HLA class II binding antigen epitope peptide #163.

Human leucocyte antigen, HLA class II; antigen epitope; pharmaceutical, immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.

OS unidentified.

PN WO9961916-A1

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PD 02-DEC-1999.

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PR 38-MAY-1999. 99WQ-TIS012066

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36-MAY-1968 09115-0007193P

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XX New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.

AA  
PS  
Claim 1: Page 42; 60pp; English.

xx The present invention relates to a new pharmaceutical composition  
cc comprising a unit dose form of a peptide, or analogue, comprising an  
cc epitope selected from those represented by peptides AY9812-19939 which  
cc are derived from various antigens for various human leucocyte antigen  
cc class DR molecules, representative of the world wide population. The

CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
CC helper T cell response. The pharmaceutical focuses the immune response  
CC towards selected determinants and could therefore be used in cases of  
CC chronic viral diseases and cancer. Examples of diseases that can be  
CC treated using the peptide containing pharmaceutical include autoimmune  
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, post-  
CC streptococcal endocarditis or glomerulonephritis and food  
CC hypersensitivities. The peptide epitopes can be used to enhance immune  
CC responses against other immunogens administered with the peptides.  
CC Diseases which can be treated using immunogenic mixtures include prostate  
CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
CC used to make monoclonal antibodies useful as potential diagnostic or  
CC therapeutic agents. The peptides may also be useful as diagnostic  
CC reagents, for example, to determine the susceptibility of an individual  
CC to a treatment regimen. Also, the peptides may be used to predict which  
CC individuals will be at substantial risk of developing chronic infection.  
CC The selection of appropriate T and B cell epitopes should allow the  
CC development of epitope based vaccines particularly towards conserved  
CC epitopes of pathogens which are characterized by high sequence  
CC variability such as HIV, HCV and Malaria  
CC  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TVPLPSETDGYVAPL 157  
| | | | | | | | | | | | | | | | | |  
Db 1 TVPLPSETDGYVAPL 15

## RESULT 24

AAG8728  
ID AAG8728 standard; peptide; 15 AA.

XX AAG8728;

DT 11-SEP-2001 (first entry)

DE HER2/NEU DR 3a motif binding peptide exemplary sequence #12.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033591.

XX 10-DEC-1999; 99US-00458299.

XX (EPI-M-) EPIMUNE INC.

XX PI Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;

XX WPI; 2001-374995/39.

XX DR

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.

XX Disclosure; Page 174; 1999P; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).

CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising  
CC a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (I) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG8726 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
CC  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TVPLPSETDGYVAPL 157  
| | | | | | | | | | | | | | | | | |  
Db 1 TVPLPSETDGYVAPL 15

## RESULT 25

AAG89108  
ID AAG89108 standard; peptide; 15 AA.

XX AAG89108;

DT 11-SEP-2001 (first entry)

DE HER2/neu DR3 binding peptide #43.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033591.

XX 10-DEC-1999; 99US-00458299.

XX (EPI-M-) EPIMUNE INC.

XX PI Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;

XX WPI; 2001-374995/39.

XX DR

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.

XX Example 5; Page 192; 1999P; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 TVPLPSETDGYVAPL 157  
Db 1 TVPLPSETDGYVAPL 15

RESULT 26  
AAG88326  
ID AAG88326 standard; peptide; 15 AA.  
XX  
AC AAG88326;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #19.  
XX  
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; cancer; cytotoxic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh B;  
XX  
DR WPI, 2001-374995/39.  
XX  
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.

XX Disclosure; Page 166; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 DGDLGWGAAGKGLQSL 127  
Db 1 DGDLGWGAAGKGLQSL 15

RESULT 27  
AAG88362  
ID AAG88362 standard; peptide; 15 AA.  
XX  
AC AAG88362;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #37.  
XX  
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; cancer; cytotoxic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141787-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000MO-US033591.  
XX  
PR 10-DEC-1999; 99US-00458299.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh B;  
XX  
DR WPI, 2001-374995/39.  
XX

PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
PS Disclosure; Page 166; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAC88266 to AAC89121 represent amino acid sequences used in  
CC the exemplification of the present invention

XX Sequence 15 AA;

XX Query Match 6.4%; Score 15; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 190 GATLERPKTSLSPGKN 204

DB 1 GATLERPKTSLSPGKN 15

RESULT 28

AAAG89099 ID AAC89099 standard; peptide; 15 AA.

XX AAC89099;

DT 11-SEP-2001 (first entry)

XX HER2/neu DR3 binding peptide #34.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;

XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;

XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

PN WO200141787-A1.

PD 14-JUN-2001.

PF 11-DEC-2000; 2000WO-US033591.

PR 10-DEC-1999; 99US-00458299.

XX (EPIM-) EPIMUNE INC.

XX Files J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI Keogh E;

DR WPI; 2001-374995/39.

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.

XX Example 5; Page 192; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
CC culture in vitro and binds to a complex of an epitope (I), bound to a  
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
CC and a second epitope and the peptide is less than 50 contiguous amino  
CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
CC and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
CC (III) are useful for inducing cellular immune responses for the  
CC prevention and treatment of cancer. (I) and (II) are useful for  
CC monitoring or evaluating an immune response to a tumour-associated  
CC antigen when incubated with a T lymphocyte sample from a patient and  
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
CC based vaccines mean that immunosuppressive epitopes that may be present  
CC in whole antigens may be avoided. Selected epitopes may be combined to  
CC enhance immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigen is eliminated. The vaccine  
CC provides the ability to direct and focus an immune response to multiple  
CC selected antigens from the same pathogen. Epitope-based anti-tumour  
CC vaccines provides the opportunity to combine epitopes derived from  
CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AAC88266 to AAC89121 represent amino acid sequences used in  
CC the exemplification of the present invention

XX Sequence 15 AA;

XX Query Match 6.4%; Score 15; DB 4; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FSRMARDPQRFVVIO 16

DB 1 FSRMARDPQRFVVIO 15

RESULT 29

AAAG88294 ID AAC88294 standard; peptide; 15 AA.

XX AAC88294;

DT 11-SEP-2001 (first entry)

XX HER2/NEU DR supermotif binding peptide exemplary sequence #3.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;

XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;

XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

OS Synthetic.

PN WO200141787-A1.

PD 14-JUN-2001.

PF 11-DEC-2000; 2000WO-US033591.

PR 10-DEC-1999; 99US-00458299.

XX (EPIM-) EPIMUNE INC.

XX Files J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI Keogh E;

PI Keogh E;  
XX  
XX MPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 166; 199pp; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical (I)  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 121 AKGLQSLPTHDPSPL 135  
DB 1 AKGLQSLPTHDPSPL 15  
RESULT 30  
AAG88474  
ID AAG88474 standard; peptide; 15 AA.  
XX  
XX AAG88474;  
XX  
XX 11-SBP-2001 (first entry)  
XX  
XX HER2/NEU DR supermotif binding peptide exemplary sequence #93.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMUNE INC.  
XX  
PA

XX  
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
PI Keogh E;  
XX  
XX MPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 168; 199pp; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical (I)  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 135 LQRYSDPTVPVPSR 149  
DB 1 LQRYSDPTVPVPSR 15  
RESULT 31  
AAG88720  
ID AAG88720 standard; peptide; 15 AA.  
XX  
XX AAG88720;  
XX  
XX 11-SBP-2001 (first entry)  
XX  
XX HER2/NEU DR 3a motif binding peptide exemplary sequence #28.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX



XX PA (EPIM-) EPIMUNE INC.  
XX Pikes J., Sette A., Sidney J., Southwood S., Chesnut R., Celis E;  
XX P1 Keogh E;  
XX DR WPI, 2001-374995/39.  
XX  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.  
XX  
XX  
XX Disclosure; Page 174; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytotaxtic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample form a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAC88266 to AAC89121 represent amino acid sequences used in  
XX the exemplification of the present invention

XX Sequence 15 AA;

XX Query Match 6.4%; Score 15; DB 4; Length 15;  
XX Best Local Similarity 100.0%; Pred.No. 2.3e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 109 SDVFDGDLGMGAAGK 123  
XX |||||  
XX 1 SDVFPDGLGMGAAGK 15

XX Db

XX RESULT 32  
XX AAG89046  
XX ID AAG89046 standard; peptide; 15 AA.  
XX AC AAG89046;  
XX XX  
XX DT 11-SEP-2001 (first entry)  
XX DE  
XX HE2/neu DR supertype primary binding peptide #40.  
XX KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytotoxic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte, CTL.  
XX OS Homo sapiens.  
XX Synthetic.  
XX PN WO200141787-A1.  
XX PD 14-JUN-2001.  
XX PF 11-DEC-2000; 2000WO-US033591.

```

XX PR 10-DEC-1999; 99US-00458239.
XX XX (EPIM-) EPIMMUNE INC.
XX PA Pikes J, Sette A, Sidney J, Southwood S, Cheenut R, Celis E,
XX P1 Keogh E;
XX DR WPI, 2001-374995/39.
XX XX
XX PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
XX PR cellular immune responses for the prevention and treatment of cancer.
XX PS
XX XX Example 5; Page 190; 199pp; English.
XX XX
XX CC The present invention describes isolated prepared HER2/neu epitopes (I).
XX CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
XX CC culture in vitro and binds to a complex of an epitope (I), bound to a
XX CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
XX CC and a second epitope and the peptide is less than 50 contiguous amino
XX CC acids that have 100% identity with a native peptide sequence of HER2/neu;
XX CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
XX CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
XX CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
XX CC immunostimulant activities, and can be used in vaccines. (I), (II) and
XX CC (III) are useful for inducing cellular immune responses for the
XX CC prevention and treatment of cancer. (I) and (II) are useful for
XX CC monitoring or evaluating an immune response to a tumour-associated
XX CC antigen when incubated with a T lymphocyte sample from a patient and
XX CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
XX CC based vaccines mean that immunosuppressive epitopes that may be present
XX CC in whole antigens may be avoided. Selected epitopes may be combined to
XX CC enhance immunogenicity. The possible pathological side effects caused by
XX CC infectious agents or whole protein antigen is eliminated. The vaccine
XX CC provides the ability to direct and focus an immune response to multiple
XX CC selected antigens from the same pathogen. Epitope-based anti-tumour
XX CC vaccines provides the opportunity to combine epitopes derived from
XX CC multiple tumour-associated molecules addressing the problem of tumour-
XX CC tumour variability and reducing the likelihood of tumour escape due to
XX CC antigen loss. AAC88266 to AAC89121 represent amino acid sequences used in
XX CC the exemplification of the present invention
XX CC
XX SQ Sequence 15 AA;
XX
XX Query Match 6.4%; Score 15; DB 4; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 168 QPDVPPPPSPRSGP 182
XX |||||
XX |||||
XX |||||
XX Db 1 QPDVPPPPSPRSGP 15
XX
XX RESULT 33
XX ID AAC88360 AAC88360
XX AC AAC88360;
XX XX
XX DE 11-SEP-2001 (first entry)
XX XX
XX DE HER2/NEU DR supermotif binding peptide exemplary sequence #36.
XX XX
XX KW Human, HER2/neu, epitope; human leukocyte antigen; HLA; T cell;
XX KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
XX KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200141787-A1.
XX XX
XX 14-JUN-2001.

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XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogn E;  
XX WPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 166; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I) bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
XX Sequence 15 AA:  
SQ  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 FVVIQNEIDLGPASPL 26  
DB 1 FVVIQNEIDLGPASPL 15  
RESULT 34  
AAG88518  
ID AAG88518 standard; peptide; 15 AA.  
XX  
XX AAG88518;  
AC  
XX 11-SEP-2001 (first entry)  
DT  
XX  
XX HER2/NEU DR supermotif binding peptide exemplary sequence #115.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
XX OS Synthetic.  
XX PN WO200141787-A1.

XX 14-JUN-2001.  
XX  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogn E;  
XX WPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 170; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I) bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
XX Sequence 15 AA:  
SQ  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 204 NGVVKDVFARFAGAVE 218  
DB 1 NGVVKDVFARFAGAVE 15  
RESULT 35  
AAG88590  
ID AAG88590 standard; peptide; 15 AA.  
XX  
XX AAG88590;  
AC  
XX 11-SEP-2001 (first entry)  
DT  
XX  
XX HER2/NEU DR supermotif binding peptide exemplary sequence #151.  
XX  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo sapiens.  
XX OS Synthetic.

XX WO200141787-A1.  
 XX 14-JUN-2001.  
 XX 11-DEC-2000; 2000WO-US033591.  
 XX 10-DEC-1999; 99US-00458299.  
 XX (EPIM-) EPIMUNE INC.  
 XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E,  
 XX Keogh E;  
 XX WPI; 2001-374995/39.  
 XX  
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 XX cellular immune responses for the prevention and treatment of cancer.  
 XX  
 XX Disclosure; Page 172; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 XX culture in vitro and binds to a complex of an epitope (I), bound to a  
 XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 XX and a second epitope and the peptide is less than 50 contiguous amino  
 XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
 XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytosolic and  
 XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
 XX (III) are useful for inducing cellular immune responses for the  
 XX prevention and treatment of cancer. (I) and (II) are useful for  
 XX monitoring or evaluating an immune response to a tumour-associated  
 XX antigen when incubated with a T lymphocyte sample from a patient and  
 XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 XX based vaccines mean that immunosuppressive epitopes that may be present  
 XX in whole antigens may be avoided. Selected epitopes may be combined to  
 XX enhance immunogenicity. The possible pathological side effects caused by  
 XX infectious agents or whole protein antigen is eliminated. The vaccine  
 XX provides the ability to direct and focus an immune response to multiple  
 XX selected antigens from the same pathogen. Epitope-based anti-tumour  
 XX vaccines provides the opportunity to combine epitopes derived from  
 XX multiple tumour-associated molecules addressing the problem of tumour-  
 XX tumour variability and reducing the likelihood of tumour escape due to  
 XX antigen loss. AA688266 to AA689121 represent amino acid sequences used in  
 XX the exemplification of the present invention  
 XX  
 XX Sequence 15 AA;  
 XX

Query Match 6.4%; Score 15; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSLLEDDDWGDLVDA 46  
 |||||  
 DB 1 RSLLEDDDWGDLVDA 15

RESULT 36  
 AA688514  
 ID AA688514 standard; peptide; 15 AA.  
 AC  
 XX AA688514;  
 XX  
 XX 11-SEP-2001 (first entry)  
 XX  
 XX HER2/NEU DR supermotif binding peptide exemplary sequence #113.  
 XX  
 XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX WO200141787-A1.  
 XX 14-JUN-2001.  
 XX 11-DEC-2000; 2000WO-US033591.  
 XX 10-DEC-1999; 99US-00458299.  
 XX (EPIM-) EPIMUNE INC.  
 XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E,  
 XX Keogh E;  
 XX WPI; 2001-374995/39.  
 XX  
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 XX cellular immune responses for the prevention and treatment of cancer.  
 XX  
 XX Disclosure; Page 170; 199pp; English.

XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 XX culture in vitro and binds to a complex of an epitope (I), bound to a  
 XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 XX and a second epitope and the peptide is less than 50 contiguous amino  
 XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
 XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytosolic and  
 XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
 XX (III) are useful for inducing cellular immune responses for the  
 XX prevention and treatment of cancer. (I) and (II) are useful for  
 XX monitoring or evaluating an immune response to a tumour-associated  
 XX antigen when incubated with a T lymphocyte sample from a patient and  
 XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 XX based vaccines mean that immunosuppressive epitopes that may be present  
 XX in whole antigens may be avoided. Selected epitopes may be combined to  
 XX enhance immunogenicity. The possible pathological side effects caused by  
 XX infectious agents or whole protein antigen is eliminated. The vaccine  
 XX provides the ability to direct and focus an immune response to multiple  
 XX selected antigens from the same pathogen. Epitope-based anti-tumour  
 XX vaccines provides the opportunity to combine epitopes derived from  
 XX multiple tumour-associated molecules addressing the problem of tumour-  
 XX tumour variability and reducing the likelihood of tumour escape due to  
 XX antigen loss. AA688266 to AA689121 represent amino acid sequences used in  
 XX the exemplification of the present invention  
 XX  
 XX Sequence 15 AA;  
 XX

Query Match 6.4%; Score 15; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NEDLGPAAPLDSTFY 31  
 |||||  
 DB 1 NEDLGPAAPLDSTFY 15

RESULT 37  
 AA688540  
 ID AA688540 standard; peptide; 15 AA.  
 AC  
 XX AA688540;  
 XX  
 XX 11-SEP-2001 (first entry)  
 XX  
 XX HER2/NEU DR supermotif binding peptide exemplary sequence #126.  
 XX  
 XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 XX

KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000WO-US033591.  
XX 10-DEC-1999; 99US-00458299.  
XX (EPIM-) EPIMUNE INC.  
XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
PI Keogh E;  
XX WPI; 2001-374995/39.  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX Disclosure; Page 170; 1999p; English.  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (1)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred.No. 2.3e-06; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 0;  
QY 163 PERYNOPDVPRPPS 177  
DB 1 PERYNOPDVPRPPS 15

RESULT 38  
AAG88558  
ID AAG88558 standard; peptide; 15 AA.  
XX  
AC AAG88558;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #135.  
XX

KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
KM tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000WO-US033591.  
XX 10-DEC-1999; 99US-00458299.  
XX (EPIM-) EPIMUNE INC.  
XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
PI Keogh E;  
XX WPI; 2001-374995/39.  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
PT cellular immune responses for the prevention and treatment of cancer.  
XX Disclosure; Page 170; 1999p; English.  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (1)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred.No. 2.3e-06; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 0;  
QY 54 QGFPCPDPAAGAGM 68  
DB 1 QGFPCPDPAAGAGM 15

RESULT 39  
AAG88672  
ID AAG88672 standard; peptide; 15 AA.  
XX  
AC AAG88672;  
XX  
DT 11-SEP-2001 (first entry)  
XX

DE HER2/NEU DR 3a motif binding peptide exemplary sequence #4.  
XX  
XX Human, HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; tumour; cancer; cytotoxic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 174; 1999p; English.  
XX  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA:  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 DLTGLPSESEAPR 98  
DB 1 DLTGLPSESEAPR 15  
RESULT 40  
AAG88684  
ID AAG88684 standard; peptide; 15 AA.  
XX  
XX AAG88684;  
XX

DT 11-SEP-2001 (first entry)  
XX  
XX HER2/NEU DR 3a motif binding peptide exemplary sequence #10.  
XX  
XX Human, HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
KW immune response; vaccine; tumour; cancer; cytotoxic; immunostimulant;  
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX  
OS Homo sapiens.  
XX Synthetic.  
XX  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 174; 1999p; English.  
XX  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be combined to  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA:  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 FVIONEDLGPASPL 26  
DB 1 FVIONEDLGPASPL 15  
RESULT 41  
AAG88566  
ID AAG88566 standard; peptide; 15 AA.  
XX  
XX AAG88566;  
XX

AC AAG88566;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #139.  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immunoreactive; vaccine; cancer; cytotoxic T lymphocyte; CTL.  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
OS Homo sapiens.  
OS Synthetic.  
XX MO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000MO-US033591.  
XX 10-DEC-1999; 99US-00458299.  
XX (BPIV-) EPIMUNE INC.  
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogh E;  
XX WPI, 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 170; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID AAG88682 standard; peptide; 15 AA.  
XX  
AC AAG88682;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE HER2/NEU DR 3a motif binding peptide exemplary sequence #9.  
XX  
KM Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX immunoreactive; vaccine; cancer; cytotoxic T lymphocyte; CTL.  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
OS Homo sapiens.  
OS Synthetic.  
XX MO200141787-A1.  
XX 14-JUN-2001.  
XX 11-DEC-2000; 2000MO-US033591.  
XX 10-DEC-1999; 99US-00458299.  
XX (BPIV-) EPIMUNE INC.  
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogh E;  
XX WPI, 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 174; 1999p; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX tumour variability and reducing the likelihood of tumour escape due to  
XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
XX the exemplification of the present invention  
XX  
SQ Sequence 15 AA;  
Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 1 TGGYVAPLTCSPQPE 15

## RESULT 45

AA689109 standard; peptide; 15 AA.

AA689109;

11-SEP-2001 (first entry)

HER2/neu DR3 binding peptide #44.

Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell; immune response; vaccine; tumour; cancer; cytotoxic T lymphocyte; CTL. tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

Homo sapiens.

Synthetic.

WO200141787-A1.

14-JUN-2001.

11-DEC-2000; 2000WO-US033591.

10-DEC-1999; 99US-00458299.

(EPIM-) EPIMMUNE INC.

Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E; Keogh E;

WPI; 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.

Example 5; Page 192; 1999P; English.

The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I) bound to a human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1) and a second epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (III) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I) and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines. (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (II) are useful for monitoring or evaluating an immune response to a tumour-associated antigen when incubated with a T lymphocyte sample from a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-antigen loss. AA689109 to AA689121 represent amino acid sequences used in the exemplification of the present invention

Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 KNGVVDVPAFGAAV 217  
Db 1 KNGVVDVPAFGAAV 15

AA689100 standard; peptide; 15 AA.

AA689100;

11-SEP-2001 (first entry)

HER2/neu DR3 binding peptide #35.

Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell; immune response; vaccine; tumour; cancer; cytotoxic T lymphocyte; CTL. tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

Homo sapiens.

Synthetic.

WO200141787-A1.

14-JUN-2001.

11-DEC-2000; 2000WO-US033591.

10-DEC-1999; 99US-00458299.

(EPIM-) EPIMMUNE INC.

Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E; Keogh E;

WPI; 2001-374995/39.

An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.

Example 5; Page 192; 1999P; English.

The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I) bound to a human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1) and a second epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (III) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I) and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines. (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (II) are useful for monitoring or evaluating an immune response to a tumour-associated antigen when incubated with a T lymphocyte sample from a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-antigen loss. AA689100 to AA689121 represent amino acid sequences used in the exemplification of the present invention

Sequence 15 AA;

Query Match 6.4%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







XX Sequence 15 AA; Score 15; DB 4; Length 15;  
SQ Query Match 6.4%; Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 DLTGLPEPSREAPR 98  
Db 1 DLTGLPEPSREAPR 15  
RESULT 49  
AAG88346  
ID AAG88346 standard; peptide; 15 AA.  
XX AAG88346;  
XX  
XX  
XX 11-SRP-2001 (first entry)  
DT  
XX  
XX HER2/NEU DR supermotif binding peptide exemplary sequence #29.  
DE  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX Immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Disclosure; Page 166; 199pp; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from  
XX multiple tumour-associated molecules addressing the problem of tumour-  
XX CC tumour variability and reducing the likelihood of tumour escape due to

CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX  
XX  
XX Sequence 15 AA; Score 15; DB 4; Length 15;  
SQ Query Match 6.4%; Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 180 EGPLPAPRPAGATLE 194  
Db 1 EGPLPAPRPAGATLE 15  
RESULT 50  
AAG89104  
ID AAG89104 standard; peptide; 15 AA.  
XX AAG89104;  
XX  
XX  
XX 11-SRP-2001 (first entry)  
DT  
XX  
XX HER2/NEU DR3 binding peptide #39.  
DE  
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
XX Immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200141787-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000MO-US033591.  
XX  
XX 10-DEC-1999; 99US-00458299.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Pike J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
XX Keogh E;  
XX WPI; 2001-374995/39.  
XX  
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
XX cellular immune responses for the prevention and treatment of cancer.  
XX  
XX Example 5; Page 192; 199pp; English.  
XX  
XX The present invention describes isolated prepared HER2/neu epitopes (I).  
XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
XX culture in vitro and binds to a complex of an epitope (I), bound to a  
XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (1)  
XX and a second epitope and the peptide is less than 50 contiguous amino  
XX acids that have 100% identity with a native peptide sequence of HER2/neu;  
XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
XX excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
XX ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
XX immunostimulant activities, and can be used in vaccines. (I), (II) and  
XX (III) are useful for inducing cellular immune responses for the  
XX prevention and treatment of cancer. (I) and (II) are useful for  
XX monitoring or evaluating an immune response to a tumour-associated  
XX antigen when incubated with a T lymphocyte sample from a patient and  
XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
XX based vaccines mean that immunosuppressive epitopes that may be present  
XX in whole antigens may be avoided. Selected epitopes may be combined to  
XX enhance immunogenicity. The possible pathological side effects caused by  
XX infectious agents or whole protein antigen is eliminated. The vaccine  
XX provides the ability to direct and focus an immune response to multiple  
XX selected antigens from the same pathogen. Epitope-based anti-tumour  
XX vaccines provides the opportunity to combine epitopes derived from

CC multiple tumour-associated molecules addressing the problem of tumour-  
CC tumour variability and reducing the likelihood of tumour escape due to  
CC antigen loss. AG68266 to AG69121 represent amino acid sequences used in  
CC the exemplification of the present invention  
XX

SO Sequence 15 AA;

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Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 QGFPCDPAPGAGM 68  
|||  
Db 1 QGFPCDPAPGAGM 15

Search completed: January 18, 2006, 20:47:41  
Job time : 81 secs